

SEARCH REQUEST FORM

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Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

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Vendors

_____ IG Suite

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_____ Other _____

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OM protein - protein search, using sw model

Run on: December 4, 2002, 10:06:40 ; Search time 42 Seconds

(without alignments)
1817.919 Million cell updates/sec

Title: US-09-869-877-10

Sequence: 1 QQSCTFSPNRACWTGTYDIN.....KSDSLKRWVEGEMLYKA 573

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 segs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: A_Geneseq_101002:*
2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
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20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 3158 | 100.0 | 573 | AAW76315 | Myceliophthora the |
| 2 | 3158 | 100.0 | 573 | AAW59913 | Myceliophthora the |
| 3 | 3158 | 100.0 | 573 | AAW62503 | Myceliophthora the |
| 4 | 3158 | 100.0 | 573 | AAW51782 | Myceliophthora the |
| 5 | 3158 | 100.0 | 573 | AAW63124 | Myceliophthora the |
| 6 | 3158 | 100.0 | 573 | AAW91085 | Myceliophthora the |
| 7 | 3158 | 100.0 | 620 | AAW85500 | Myceliophthora lac |
| 8 | 3158 | 100.0 | 620 | AAW16302 | Myceliophthora lac |
| 9 | 3158 | 100.0 | 620 | AAW50729 | M. thermophila lac |
| 10 | 3140 | 99.4 | 573 | AAW79079 | Myceliophthora the |

| | | | | | |
|----|--------|------|-----|----------|--------------------|
| 11 | 3124 | 98.9 | 620 | AAW19855 | Myceliophthora the |
| 12 | 3118 | 98.7 | 573 | AAW76317 | Myceliophthora the |
| 13 | 3118 | 98.7 | 573 | AAW79078 | Myceliophthora the |
| 14 | 3112 | 98.5 | 573 | AAW76316 | Myceliophthora the |
| 15 | 3112 | 98.5 | 573 | AAW79077 | Myceliophthora the |
| 16 | 2428.5 | 76.9 | 623 | AAW76464 | Melanocarpus albon |
| 17 | 2096.5 | 66.4 | 616 | AAW18060 | Scybalidium thermo |
| 18 | 2076.5 | 65.8 | 616 | AAW76314 | Scybalidium thermo |
| 19 | 2076.5 | 65.8 | 616 | AAW59915 | Scybalidium thermo |
| 20 | 2076.5 | 65.8 | 616 | AAW62502 | Scybalidium thermo |
| 21 | 2076.5 | 65.8 | 616 | AAW51783 | Scybalidium thermo |
| 22 | 2076.5 | 65.8 | 616 | AAW91086 | Scybalidium thermo |
| 23 | 1071.5 | 33.9 | 581 | AAW76443 | Novel Botrytis cin |
| 24 | 638 | 20.2 | 499 | AAW76295 | Polyporus pinus |
| 25 | 636 | 20.1 | 499 | AAW76295 | Polyporus pinus |
| 26 | 636 | 20.1 | 499 | AAW60875 | Polyporus pinus |
| 27 | 636 | 20.1 | 520 | AAW90721 | Polyporus pinus |
| 28 | 636 | 20.1 | 520 | ABW77510 | Laccase-LCC1. Pol |
| 29 | 635 | 20.1 | 499 | AAW76297 | Trametes versicolo |
| 30 | 630 | 19.9 | 499 | AAW76296 | Polyporus pinus |
| 31 | 629 | 19.9 | 499 | AAW76298 | Polyporus pinus |
| 32 | 620.5 | 19.6 | 518 | AAW61387 | Schizophyllum comm |
| 33 | 615 | 19.5 | 499 | AAW7069 | Phenol oxidase (PO |
| 34 | 614 | 19.4 | 499 | AAW05279 | Amino acid sequenc |
| 35 | 614 | 19.4 | 499 | AAW07068 | Phenol oxidase (PO |
| 36 | 614 | 19.4 | 539 | AAW17973 | Coprinus cinereus |
| 37 | 614 | 19.4 | 539 | AAW76281 | Coprinus cinereus |
| 38 | 614 | 19.4 | 539 | AAW60874 | Coprinus cinereus |
| 39 | 611.5 | 19.4 | 524 | AAW92810 | Coprinus cinereus |
| 40 | 609.5 | 19.3 | 529 | AAW76310 | T. versicolor lacc |
| 41 | 609.5 | 19.3 | 529 | AAW60878 | Rhizoctonia solani |
| 42 | 609.5 | 19.3 | 529 | AAW50728 | R. solani laccase |
| 43 | 607.5 | 19.2 | 529 | AAW16301 | Rhizoctonia solani |
| 44 | 603.5 | 19.1 | 529 | AAW72328 | Laccase R51ac3. R |
| 45 | 601.5 | 19.0 | 511 | AAW90724 | Laccase-LCC4. Pol |

ALIGNMENTS

RESULT 1
ID AAW76315 standard; protein: 573 AA.
XX AAW76315;
AC AAW76315;
XX 08-JAN-1999 (first entry)
DT
XX
DE Myceliophthora thermophila laccase protein.
XX
XX Laccase; variant; oxidation; dye transfer inhibition; bleaching;
KW denim; lignin modification; paper strengthening; phenol polymerisation;
KW hair dye; waste water treatment.
XX
XX
OS Myceliophthora thermophila.
XX
XX W09838287-A1.
XX
XX 03-SEP-1998.
XX
XX 23-FEB-1998; 98W0-DK00070.
XX
XX 28-FEB-1997; 97DK-0000222.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Svendsen A, Xu F;
XX
XX WPT; 1998-495393/42.
XX
XX
XX New variants of Coprinus and related laccases with increased
XX oxidation potential - or altered pH optimum, or mediator or
XX oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting

QY 481 LPAFGWVYLSFRADNGALFHCCHIAHVSGLGVYTLERADDLRGAVSDADADLDRLC 540
 DB 481 LPAFGWVYLSFRADNGALFHCCHIAHVSGLGVYTLERADDLRGAVSDADADLDRLC 540
 QY 541 ADMRRYPTNPYKPSDGLKHHRVGECEWLVKA 573
 DB 541 ADMRRYPTNPYKPSDGLKHHRVGECEWLVKA 573
 RESULT 3
 AAM62503
 ID AAM62503 standard; Protein; 573 AA.
 XX
 AC AAM62503;
 XX
 DT 09-NOV-1998 (first entry)
 XX
 DE Mycellophthora thermophila laccase.
 XX
 KM Coprinus laccase-like enzyme; enzyme engineering; enzyme stability;
 KM detergent; bleaching.
 XX
 OS Mycellophthora thermophila.
 XX
 FH Key
 FH Location/Qualifiers
 FT Misc-difference 433
 FT "variant may have Ala, Val, Leu, Ile, Pro,
 FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,
 FT Gln, Asp, Glu, Lys, Arg or His (preferably
 FT Phe, Val, Ile, Leu or Gln) at this
 FT position"
 FT Misc-difference 373
 FT "variant may have Ala, Val, Leu, Ile, Pro,
 FT Phe, Met, Gly, Ser, Thr, Cys, Tyr, Asn,
 FT Gln, Asp, Glu, Lys, Arg or His (preferably
 FT Phe or His) at this position"
 FT Misc-difference 136
 FT "variant may have Ala, Val, Leu, Ile, Pro,
 FT Phe, Met, Gly, Ser, Thr, Cys, Tyr, Asn,
 FT Gln, Asp, Glu, Lys, Arg or His (preferably
 FT Phe or His) at this position"
 FT Misc-difference 145
 FT "variant may have Ala, Val, Leu, Ile, Pro,
 FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
 FT Gln, Asp, Glu, Lys, Arg or His (preferably
 FT Phe or His) at this position"
 FT Misc-difference 480
 FT "variant may have Ala, Val, Leu, Ile, Pro,
 FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,
 FT Gln, Asp, Glu, Lys, Arg or His (preferably
 FT Phe, Val, Ile, Leu or Gln) at this
 FT position"
 FT Misc-difference 137
 FT "variant may have Ala, Val, Leu, Ile, Pro,
 FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
 FT Gln, Asp, Glu, Lys, Arg or His (preferably
 FT Phe) at this position"
 FT Misc-difference 176
 FT "variant may have Ala, Val, Leu, Ile, Pro,
 FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
 FT Gln, Asp, Glu, Lys, Arg or His (preferably
 FT Phe) at this position"
 FT Misc-difference 254
 FT "variant may have Ala, Val, Leu, Ile, Pro,
 FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,
 FT Gln, Asp, Glu, Lys, Arg or His (preferably
 FT Phe, Val, Ile, Leu or Gln) at this
 FT position"
 XX
 FN W09827198-AL.
 XX
 PD 25-JUN-1998.

XX
 PF 16-DEC-1997; 97WO-DK00571.
 XX
 PR 08-SEP-1997; 97DK-0001021.
 PR 19-DEC-1996; 96DK-0001449.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Cherry JR, Pedersen AH, Rasmussen G, Schneider P;
 PI Svendsen A;
 DR WPI; 1998-362768/31.
 XX
 PT New laccase variants with improved stability - having amino acid
 PT changes based on Coprinus laccase structure, used for e.g.
 PT oxidation, dye transfer inhibition or bleaching
 XX
 PS Claim 18; 156-157; 168pp; English.
 XX
 CC This is a laccase enzyme of Mycellophthora thermophila. The
 CC invention relates to the design of new variants of Coprinus-like
 CC laccases (see AAM60874-79, AAM60925 and AAM62501-03); this M.
 CC thermophila laccase shows 56.5% homology to C. cinereus laccase. The
 CC modifications are based on the previously unknown three-dimensional
 CC structure of C. cinereus laccase. Amino acid residues identified as
 CC being important to protein stability are identified and altered to
 CC improve stability. The variants are typically obtained by
 CC mutagenesis of laccase DNA and expression in a host cell. Variants
 CC are preferably modified within 15 (especially 10 or 5) Angstrom
 CC of a copper ion in the three-dimensional structure of the laccase.
 CC For M. thermophila laccase variants, preferred substitutions are
 CC one or more of W433F/V/I/L/Q, W373F/H, W136F/H, Y145F,
 CC M480F/V/I/L/Q, Y137F, Y176F and M254F/V/I/L/Q. The stabilised
 CC laccase variants can be used in detergent additives, for dye
 CC transfer inhibition in detergents, in bleaching of textiles (in
 CC particular denim), for lignin modification, paper strengthening,
 CC phenol polymerisation, hair dyeing and in waste water treatment.
 XX
 SQ Sequence 573 AA;
 Query Match 100.0%; Score 3158; DB 19; Length 573;
 Best local Similarity 100.0%; Pred. No. 7.6e-276;
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QOSCNTPSNACWTDGIDITDYEDSDPTGVVRYTLTLEVDNMTGPGVYKEMVLY 60
 DB 1 QOSCNTPSNACWTDGIDITDYEDSDPTGVVRYTLTLEVDNMTGPGVYKEMVLY 60
 QY 61 NNSIIGPTTFADMGDTIQTQVIVNNLETNGSIHHMGLHOKGTNLHDANGITTECPPIPKG 120
 DB 61 NNSIIGPTTFADMGDTIQTQVIVNNLETNGSIHHMGLHOKGTNLHDANGITTECPPIPKG 120
 QY 121 GRRVYRFAKQOYGTSMVSHFSQAQYNGVGAIOINGPASPVDYTDGVEPISDYSSA 180
 DB 121 GRRVYRFAKQOYGTSMVSHFSQAQYNGVGAIOINGPASPVDYTDGVEPISDYSSA 180
 QY 122 GRVYRFAKQOYGTSMVSHFSQAQYNGVGAIOINGPASPVDYTDGVEPISDYSSA 180
 DB 122 GRVYRFAKQOYGTSMVSHFSQAQYNGVGAIOINGPASPVDYTDGVEPISDYSSA 180
 QY 181 DELVELTKNSGAPSDNVLENGTAKHETGEGERANTTLPGRRRLRLINTSVENHOV 240
 DB 181 DELVELTKNSGAPSDNVLENGTAKHETGEGERANTTLPGRRRLRLINTSVENHOV 240
 QY 181 DELVELTKNSGAPSDNVLENGTAKHETGEGERANTTLPGRRRLRLINTSVENHOV 240
 DB 181 DELVELTKNSGAPSDNVLENGTAKHETGEGERANTTLPGRRRLRLINTSVENHOV 240
 QY 241 SLVNHMCIITAAAMPVNAATVDSLFLFGVGORVDVYEARTPENYFNTPFGGLICGG 300
 DB 241 SLVNHMCIITAAAMPVNAATVDSLFLFGVGORVDVYEARTPENYFNTPFGGLICGG 300
 QY 301 SRNPYPAIFHYAGAGPGPTDEGKAPVNDNCIDLPMLKBPVAVDVLSGFAKADNTLD 360
 DB 301 SRNPYPAIFHYAGAGPGPTDEGKAPVNDNCIDLPMLKBPVAVDVLSGFAKADNTLD 360
 QY 361 VTLDITGTPLFPVKKVNSAINDMGRVVDVYLTQNTSFPFGYIVVEVNGADQSYLIE 420
 DB 361 VTLDITGTPLFPVKKVNSAINDMGRVVDVYLTQNTSFPFGYIVVEVNGADQSYLIE 420
 QY 421 NDGCAFTLPHPHLHGHDFYVILGRSPDESASNERHVPDPADAGLLSGANPVRDVS 480
 DB 421 NDGCAFTLPHPHLHGHDFYVILGRSPDESASNERHVPDPADAGLLSGANPVRDVS 480

XX AAM63124;
 AC 12-OCT-1998 (first entry)
 DT
 DE Myceliophthora thermophila laccase protein.
 XX
 XX
 KM Laccase protein; variant; lignin modification; paper strengthening;
 KM dye transfer inhibition; phenol2 polymerisation; hair dyeing;
 KM textile bleaching; denim; waste water treatment.
 XX
 OS Myceliophthora thermophila.
 FH
 XX
 XX Key Location/Qualifiers
 PN W09827197-A1.
 PD 25-JUN-1998.
 XX
 XX 12-DEC-1997; 97MO-DK00566.
 PF
 XX 08-SEP-1997; 97DK-0001020.
 PR 19-DEC-1996; 96DK-0001450.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Cherry JR, Pedersen AH, Rasmussen G, Schneider P;
 PI Svendsen A;
 DR WPI; 1998-362767/31.
 XX
 XX New laccase variants - have amino acid changes in Myceliophthora or
 PT Scybalidium laccase(s), used for e.g. oxidation, dye transfer
 PT Inhibition or bleaching
 PS
 XX
 PS Claim 1: Pages 18-21; 30pp; English.
 CC
 CC The present sequence represents a laccase protein. The sequence is used
 CC to construct laccase variants (AAM63124-27, AAM63129-32 and AAM63135),
 CC which have improved stability as compared to the parent laccase, and
 CC comprises a mutation in tyrosine, tryptophan or methionine residues. The
 CC laccase variants can be used for e.g. lignin modification, paper
 CC strengthening, dye transfer inhibition in detergents, phenol
 CC polymerisation, hair dyeing, bleaching of textiles (in particular
 CC bleaching of denim) and waste water treatment.
 CC
 XX
 SQ Sequence 573 AA;
 Query Match 100.0%; Score 3158; DB 19; Length 573;
 Best Local Similarity 100.0%; Pred. No. 7, 6e-276;
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLFKVVADVPLSGFAKRAADTLD 360
 OY 361 VTIDTGTGTPLEFWKVNKSAINIDMGRAVDYVLTQNTSPFGYNIIVEKNADQSYLIE 420
 DB 361 VTIDTGTGTPLEFWKVNKSAINIDMGRAVDYVLTQNTSPFGYNIIVEKNADQSYLIE 420
 OY 421 NDGAPPTLPHPMLHGHDFYVLAGRSPESPASNERHVEDPARDAGLLSGANPYRDVSM 480
 DB 421 NDGAPPTLPHPMLHGHDFYVLAGRSPESPASNERHVEDPARDAGLLSGANPYRDVSM 480
 OY 481 LPAGWVLSFRADNPGAMLFHCHIAMHVSGLVYTLERADLRGAVSPADDDDLRLC 540
 DB 481 LPAGWVLSFRADNPGAMLFHCHIAMHVSGLVYTLERADLRGAVSPADDDDLRLC 540
 OY 541 ADMRRYPTNPYPKSDGKLRHVEEGEWLYKA 573
 DB 541 ADMRRYPTNPYPKSDGKLRHVEEGEWLYKA 573
 RESULT 6
 AAY91085
 ID AAY91085 standard; protein; 573 AA.
 XX
 AC AAY91085;
 XX
 XX 13-SEP-2000 (first entry)
 DT
 DE Myceliophthora thermophila laccase amino acid sequence SEQ ID NO:1.
 XX
 XX
 KM Laccase; polyphenol oxidase; oxidation; mutant; variant; detergent;
 KM inhibiting dye transfer; bleaching textile; lignin modification;
 KM paper strengthening; phenol polymerisation; hair dyeing;
 KM waste water treatment.
 XX
 XX Thielavia heteroythallica.
 OS
 XX
 XX US6060442-A.
 PN
 XX 09-MAY-2000.
 PD
 XX
 XX 24-FEB-1998; 98US-0028887.
 PF
 XX
 XX 24-FEB-1998; 98US-0028887.
 PR
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 XX Svendsen A;
 PI
 XX
 DR WPI; 2000-375259/32.
 XX
 PT Laccase variants for oxidizing substrate, inhibiting dye transfer and
 PT bleaching textiles has increased oxidation potential and/or changed pH
 PT and/or altered mediatory and/or altered oxygen/hydroxyl group pathways
 PT
 XX
 PS Claim 1: Column 9-12; 10pp; English.
 XX
 XX The present invention describes laccase variants (1S) with increased
 CC oxidation potential and/or changed pH optimum and/or altered mediator
 CC pathway and/or altered O2/OH- pathway. Also described are: (1) a
 CC detergent additive comprising (1) in the form of a non-dusting granule,
 CC a stabilised liquid or a protected enzyme; and (2) a detergent
 CC composition comprising (1) and a surfactant. (1) is useful for oxidising
 CC a substrate, inhibiting dye transfer and bleaching textiles. 1S are also
 CC useful for various industrial applications such as lignin modification,
 CC paper strengthening, phenol polymerisation, hair dyeing and waste water
 CC treatment. The present sequence represents the Myceliophthora thermophila
 CC (also known as Thielavia heteroythallica) laccase amino acid sequence
 CC which is modified in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 573 AA;

| | | |
|----|---|---|
| XX | | Myceliophthora thermophila laccase. |
| DE | | |
| XX | | Blue copper oxidase; laccase; enzyme engineering; |
| KW | | protein engineering; lignin depolymerisation; dye oxidation. |
| XX | | |
| XX | | Myceliophthora thermophila. |
| XX | | |
| FH | Key | Location/Qualifiers |
| FT | Peptide | 1..47 |
| FT | | /label= Sig_peptide |
| FT | Protein | 48..620 |
| FT | | /label= Mat-protein |
| FT | Binding-site | 478 |
| FT | | /note= "Type I copper site ligand" |
| FT | Binding-site | 550 |
| FT | | /note= "Type I copper site ligand" |
| FT | Binding-site | 555 |
| FT | | /note= "Type I copper site ligand" |
| FT | Binding-site | 560 |
| FT | | /note= "possible Type I copper site ligand" |
| FT | Peptide | 269..278 |
| FT | | /note= "preferred site for mutation (Claim 30), corresponds to W163 region of ascorbate oxidase |
| FT | | |
| FT | Peptide | 355..364 |
| FT | | /note= "preferred site for mutation (Claim 29), corresponds to R285 region of ascorbate oxidase" |
| FT | | |
| FT | Peptide | 408..423 |
| FT | | /note= "preferred site for mutation (Claim 28), corresponds to Q353 and W362 region of ascorbate oxidase" |
| FT | | |
| FT | Peptide | 468..480 |
| FT | | /note= "preferred site for mutation (Claim 26), contains Cu-ligating His" |
| FT | | |
| FT | Peptide | 544..562 |
| FT | | /note= "preferred site for mutation (Claim 27), contains Cu-ligating His and Cys" |
| FT | | |
| FT | Peptide | 556..560 |
| FT | | /note= "preferred site for mutation (Claim 20)" |
| XX | | |
| PN | WO9709431-A1. | |
| PD | | |
| PD | 13-MAR-1997. | |
| XX | | |
| PE | 03-SEP-1996; | 96WO-US14087. |
| XX | | |
| PR | 01-SEP-1995; | 95US-0003142. |
| XX | | |
| PA | (NOVO) NOVO NORDISK BIOTECH INC. | |
| PI | | |
| RJ | Berka RM, Wahleithner JA, Xu F, Berka R; | |
| DR | WI: 1997-192906/17. | |
| DR | N-PDSB; AAT63318. | |
| XX | | |
| PS | | |
| PT | New mutant blue copper oxidase enzymes - having different specific | |
| PT | activities to wild-type enzymes, used for e.g. lignin | |
| PT | (de)polymerisation or oxidation of dyes | |
| XX | | |
| PS | Disclosure; Fig 7A-E; 48pp; English. | |
| XX | | |
| CC | Myceliophthora thermophila laccase (AMM16302) can be engineered to | |
| CC | alter e.g. its specific activity or pH-activity profile or to | |
| CC | improve expression yields. The mutant laccase is prepd. by site- | |
| CC | directed mutagenesis of the lcc-1 gene (AAT63318) and expression in | |
| CC | host cells. The mutation may be a deletion, insertion or pref. a | |
| CC | substn. of one or more amino acids at a location no greater than | |
| CC | 12 Angstroms, pref. no more than 2.5 Angstroms, from the Type I | |
| CC | copper site. The mutant enzyme can be used e.g. for the | |
| CC | polymerisation or depolymerisation of lignins, oxidation of dyes, | |
| CC | or polymerisation of phenolic or aniline cpds. present in liquids, | |
| CC | | |

| CC | e.g. for the treatment of fruit juices. |
|----|---|
| XX | Sequence 620 AA; |
| XX | Query Match 100.0%; Score 3158; DB 18; Length 620; |
| XX | Best Local Similarity 100.0%; Pred. No. 8,56-276; |
| XX | Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0 |
| XX | 1 QOQCPTPSNRACWTDGYDINTDYEVDSPDTGVVRPTTLTLEVDNMTGPDGVKKEKMLV 60 |
| XX | 48 QOQCPTPSNRACWTDGYDINTDYEVDSPDTGVVRPTTLTLEVDNMTGPDGVKKEKMLV 107 |
| XX | 61 NNSIIGPTFEAMGDPDIQVTVINNETNSTSIHMGLHOKGNLHDGANGITECPRPKG 120 |
| XX | 108 NNSIIGPTFEAMGDPDIQVTVINNETNSTSIHMGLHOKGNLHDGANGITECPRPKG 167 |
| XX | 121 GKKVYRFEKAQQYGTSTWYSHSFSAQYGNVYGAALQINGPASPLEDYDGLVFPISDYYS 180 |
| XX | 168 GKKVYRFEKAQQYGTSTWYSHSFSAQYGNVYGAALQINGPASPLEDYDGLVFPISDYYS 227 |
| XX | 181 DELVELTKKSGAPESDNYVLENGTAKHRETGESEYANVTLPGRHRRLINTSVENHFOV 240 |
| XX | 228 DELVELTKKSGAPESDNYVLENGTAKHRETGESEYANVTLPGRHRRLINTSVENHFOV 287 |
| XX | 241 SLVNHITMCIADAMPVNMATVDSLFLVGYGORDVYIEANRTPGNITWTFEGGGLICGG 300 |
| XX | 288 SLVNHITMCIADAMPVNMATVDSLFLVGYGORDVYIEANRTPGNITWTFEGGGLICGG 347 |
| XX | 301 SNNPYPALFHNAGAGGPRPTDEGKAPVHNCLDEPLKPVYARDVPLSGFAKRDNTLD 360 |
| XX | 348 SNNPYPALFHNAGAGGPRPTDEGKAPVHNCLDEPLKPVYARDVPLSGFAKRDNTLD 407 |
| XX | 361 VILDTTGPRLFPMKVGSAINIDMGAAVVDVYLTOFTSPFGNITVEVNGADOMSTWLE 420 |
| XX | 408 VILDTTGPRLFPMKVGSAINIDMGAAVVDVYLTOFTSPFGNITVEVNGADOMSTWLE 467 |
| XX | 421 NDPGAFETLPHRMHLGHDFYVLGKSPDESPASNEHNVFDPARDAGLLSGAEVRRDVS 480 |
| XX | 468 NDPGAFETLPHRMHLGHDFYVLGKSPDESPASNEHNVFDPARDAGLLSGAEVRRDVS 527 |
| XX | 481 LEAFGVVULSFPAADNGAVLPHCHTAMHVSGLGVYLLERADLRGAVSDADADLDRLC 540 |
| XX | 528 LEAFGVVULSFPAADNGAVLPHCHTAMHVSGLGVYLLERADLRGAVSDADADLDRLC 587 |
| XX | 541 ADMRRYPTNPYPKSDSGLKHRRVGECEWLVYA 573 |
| XX | 588 ADMRRYPTNPYPKSDSGLKHRRVGECEWLVYA 620 |
| XX | RESULT 9 |
| XX | AAV50729 |
| XX | ID AAV50729 standard; Protein: 620 AA. |
| XX | AAV50729; |
| XX | AAV50729; |
| XX | 08-FEB-2000 (first entry) |
| XX | M. thermophila laccase lcc-1 protein. |
| XX | Laccase; mutant; lignin polymerization; Kraft; liganosulfate; lignin; |
| XX | depolymerization; phenol; fruit juice; dye; lcc-1. |
| XX | Myceliophthora thermophila. |
| XX | US5972670-A. |
| XX | 26-OCT-1999. |
| XX | 09-JAN-1998; 98US-0005397. |
| XX | 30-AUG-1996; 96US-0706037. |
| XX | (FENG/) FENG X. |

SO Sequence 573 AA: 99.4%; Score 3140; DB 19; Length 573;
 Query Match Best Local Similarity 99.5%; Pred. No. 3.2e-274;
 Matches 570; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QOSCTPSNRACWTDGYDINTDYEDSPDTGVRRPTLTLTLEVDNMTGPDGVYKEVMY 60
 DB 1 QOSCTPSNRACWTDGYDINTDYEDSPDTGVRRPTLTLTLEVDNMTGPDGVYKEVMY 60
 OY 61 NNSIIGPTIFADMGDTIQVTYINNETNGSTIHMGLHOKGTNLHGANGITECPPIPKG 120
 DB 61 NNSIIGPTIFADMGDTIQVTYINNETNGSTIHMGLHOKGTNLHGANGITECPPIPKG 120
 OY 121 GRKYRFRKAQOYGTSMYSHSFSAQYONGYVGAIQINGPASLPYDLDGVFPISDYYSSA 180
 DB 121 GRKYRFRKAQOYGTSMYSHSFSAQYONGYVGAIQINGPASLPYDLDGVFPISDYYSSA 180
 OY 181 DELVELTKNSGAPESDNYLFNGTAKHPETGEGEYANVTLPGRHRRLRLINTSVENHFQY 240
 DB 181 DELVELTKNSGAPESDNYLFNGTAKHPETGEGEYANVTLPGRHRRLRLINTSVENHFQY 240
 OY 241 SLVNHMTCLIAADMYPVNMTVDLSFLVGQRYDVYIEANRPENYFNTFGGGLCG 300
 DB 241 SLVNHMTCLIAADMYPVNMTVDLSFLVGQRYDVYIEANRPENYFNTFGGGLCG 300
 OY 301 SRNPYPALFHYAGAPGEPTEDEGKAPVDHNCIDLPNLKPVYARVPLSGFAKRAADNTLD 360
 DB 301 SRNPYPALFHYAGAPGEPTEDEGKAPVDHNCIDLPNLKPVYARVPLSGFAKRAADNTLD 360
 OY 361 VTLDTGTPLFWKNGSAINIDMGRAVVDYLTQNTSPPGNIYEVGAQOMSTWLE 420
 DB 361 VTLDTGTPLFWKNGSAINIDMGRAVVDYLTQNTSPPGNIYEVGAQOMSTWLE 420
 OY 421 NDPGAFETLPHPMHLGHDFYVLGRSPDESPASNERHVPDPADAGLLSGANVPRDYSK 480
 DB 421 NDPGAFETLPHPMHLGHDFYVLGRSPDESPASNERHVPDPADAGLLSGANVPRDYSK 480
 OY 481 LPAFGWVVLSPFADNPGAMLFHCHIAHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
 DB 481 LPAFGWVVLSPFADNPGAMLFHCHIAHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
 OY 541 ADMRRYWPNTNPKSDSGLKHRRVGECEWLVKA 573
 DB 541 ADMRRYWPNTNPKSDSGLKHRRVGECEWLVKA 573

RESULT 11
 AAM19855
 ID AAM19855 standard; Protein; 620 AA.
 AC AAM19855;
 DT 11-SEP-1997 (first entry)
 DE Mycellophthora thermophila laccase useful in dye composition.
 KW Laccase; dye; keratin; hair; fur; hide; wool.
 OS Mycellophthora thermophila.
 XX WO9719999-A1.
 PN 05-JUN-1997.
 PD 29-NOV-1996; 96MO-DK00499.
 PF 30-NOV-1995; 95DK-0001357.
 PR (NOVO) NOVO-NORDISK AS.
 PA Aaslyng D, Rorbaek K, Sorensen NH;
 PI
 XX

DR WPI: 1997-310565/28.
 DR N-PSDB; AAT72106.
 XX Dyeing composition for dyeing keratinous fibres, e.g. human hair. -
 PT comprises microbial laccase, dye precursor and optionally a modifier
 PS Disclosure: Page 19-22; 37pp; English.
 XX Mycellophthora thermophila laccase (AAM19855) catalyses the
 CC oxidation of phenols, resulting in the prodn. of aryloxy-radical
 CC intermediates. The ultimate coupling of these intermediates
 CC provides a combination of dimeric, oligomeric and polymeric
 CC reaction products, some of which can be used to form dyes. The
 CC enzyme can be produced in heterologous host cells, esp. filamentous
 CC fungi, yeast or bacteria, utilising vectors contg. the laccase gene
 CC (AAT72106). It is used in compositions, together with one or more
 CC dye precursors and optionally one or more modifiers, for dyeing
 CC fur, hide, wool and hair, esp. human hair. Dyeing is faster.
 CC and/or requires less enzyme and/or less precursor (some precursors
 CC are unhealthly and carcinogenic) than prior methods using oxidising
 CC enzyme and precursor.
 CC

SO Sequence 620 AA: 98.9%; Score 3124; DB 18; Length 620;
 Query Match Best Local Similarity 98.8%; Pred. No. 1e-272;
 Matches 566; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 QOSCTPSNRACWTDGYDINTDYEDSPDTGVRRPTLTLTLEVDNMTGPDGVYKEVMY 60
 DB 48 QOSCTPSNRACWTDGYDINTDYEDSPDTGVRRPTLTLTLEVDNMTGPDGVYKEVMY 107
 OY 61 NNSIIGPTIFADMGDTIQVTYINNETNGSTIHMGLHOKGTNLHGANGITECPPIPKG 120
 DB 108 NNSIIGPTIFADMGDTIQVTYINNETNGSTIHMGLHOKGTNLHGANGITECPPIPKG 167
 OY 121 GRKYRFRKAQOYGTSMYSHSFSAQYONGYVGAIQINGPASLPYDLDGVFPISDYYSSA 180
 DB 168 GRKYRFRKAQOYGTSMYSHSFSAQYONGYVGAIQINGPASLPYDLDGVFPISDYYSSA 227
 OY 181 DELVELTKNSGAPESDNYLFNGTAKHPETGEGEYANVTLPGRHRRLRLINTSVENHFQY 240
 DB 228 DELVELTKNSGAPESDNYLFNGTAKHPETGEGEYANVTLPGRHRRLRLINTSVENHFQY 287
 OY 241 SLVNHMTCLIAADMYPVNMTVDLSFLVGQRYDVYIEANRPENYFNTFGGGLCG 300
 DB 288 SLVNHMTCLIAADMYPVNMTVDLSFLVGQRYDVYIEANRPENYFNTFGGGLCG 347
 OY 301 SRNPYPALFHYAGAPGEPTEDEGKAPVDHNCIDLPNLKPVYARVPLSGFAKRAADNTLD 360
 DB 348 SRNPYPALFHYAGAPGEPTEDEGKAPVDHNCIDLPNLKPVYARVPLSGFAKRAADNTLD 407
 OY 361 VTLDTGTPLFWKNGSAINIDMGRAVVDYLTQNTSPPGNIYEVGAQOMSTWLE 420
 DB 408 VTLDTGTPLFWKNGSAINIDMGRAVVDYLTQNTSPPGNIYEVGAQOMSTWLE 467
 OY 421 NDPGAFETLPHPMHLGHDFYVLGRSPDESPASNERHVPDPADAGLLSGANVPRDYSK 480
 DB 468 NDPGAFETLPHPMHLGHDFYVLGRSPDESPASNERHVPDPADAGLLSGANVPRDYSK 527
 OY 481 LPAFGWVVLSPFADNPGAMLFHCHIAHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
 DB 528 LPAFGWVVLSPFADNPGAMLFHCHIAHVSGLGVYLLERADDLRGAVSDADADDLRLC 587
 OY 541 ADMRRYWPNTNPKSDSGLKHRRVGECEWLVKA 573
 DB 588 ADMRRYWPNTNPKSDSGLKHRRVGECEWLVKA 620

RESULT 12
 AAM76317
 ID AAM76317 standard; protein; 573 AA.
 XX

```

XX 20-FEB-1998; 98WO-DK00067.
XX 28-FEB-1997; 97DK-0000221.
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Svendsen A;
XX
XX WPI; 1998-495392/42.
XX
XX New variants of laccase with increased oxidation potential - or
XX altered pH optimum, mediator efficiency or oxygen-hydroxide ion
XX pathways, useful for oxidation, inhibiting dye transfer and in
XX textile bleaching
XX
XX Claim 4; Page -: 34pp; English.
XX
XX The laccase protein mutants AAW79077-W79079 contain one or more of the
XX above mutations and are examples of polypeptides modified from the
XX wild-type sequence by using site-directed, random, or localised random
XX mutagenesis. These mutants may have an (a) increased random
XX potential, (b) altered pH optimum, (c) altered mediator efficiency, (d)
XX altered oxygen/hydroxide ion pathway, depending on the particular
XX mutations that have occurred. This particular sequence has mutations
XX that will alter the laccase's oxygen/hydrogen ion pathway. These
XX variants can be used to oxidise substrates, inhibit dye transfer, as
XX detergent additives and bleaching textiles. They can also be used in
XX lignin modification; strengthening paper; polymerisation of phenols;
XX dyeing of hair and textiles and waste water treatment.
XX N.B. This sequence is not shown in the water treatment.
XX from the wild-type Mycellophthora thermophila laccase sequence given in
XX the specification.
XX
XX Sequence 573 AA;
XX
XX Query Match 98.7%; Score 3118; DB 19; Length 573;
XX Best Local Similarity 99.0%; Pred. No 3.1e-272;
XX Matches 567; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 QOQSCNTPSNRACWTDGYDINTDYVSDPDGVVRPYTLTLEVDNMTGPDGVKRWLV 60
XX 1 QOQSCNTPSNRACWTDGYDINTDYVSDPDGVVRPYTLTLEVDNMTGPDGVKRWLV 60
XX
XX 61 NNSITGPTIRADMGDTQOVYINLLENGTSIHNGHGLKQKTNLADGANGTTECPPIPKG 120
XX 61 NNSITGPTIRADMGDTQOVYINLLENGTSIHNGHGLKQKTNLADGANGTTECPPIPKG 120
XX
XX 61 GRYKYRKAQOYGTSWHSFSAQYNGVYGAIOINGPASLPYDTDLGVFISDIYSSA 180
XX 61 GRYKYRKAQOYGTSWHSFSAQYNGVYGAIOINGPASLPYDTDLGVFISDIYSSA 180
XX
XX 121 GRYKYRKAQOYGTSWHSFSAQYNGVYGAIOINGPASLPYDTDLGVFISDIYSSA 180
XX 121 GRYKYRKAQOYGTSWHSFSAQYNGVYGAIOINGPASLPYDTDLGVFISDIYSSA 180
XX
XX 121 GRYKYRKAQOYGTSWHSFSAQYNGVYGAIOINGPASLPYDTDLGVFISDIYSSA 180
XX 121 GRYKYRKAQOYGTSWHSFSAQYNGVYGAIOINGPASLPYDTDLGVFISDIYSSA 180
XX
XX 181 DELVELTKNSGAPSDNVLENGTAKHPEGTGEGEYANTLPLGRHRRLRLINTSVENHFOV 240
XX 181 DELVELTKNSGAPSDNVLENGTAKHPEGTGEGEYANTLPLGRHRRLRLINTSVENHFOV 240
XX
XX 181 DELVELTKNSGAPSDNVLENGTAKHPEGTGEGEYANTLPLGRHRRLRLINTSVENHFOV 240
XX 181 DELVELTKNSGAPSDNVLENGTAKHPEGTGEGEYANTLPLGRHRRLRLINTSVENHFOV 240
XX
XX 241 SLVNHPTMCITLAAMVPVNAATVLSLFGVGRYDVLEANTPBNYFNFVFGGLCGG 300
XX 241 SLVNHPTMCITLAAMVPVNAATVLSLFGVGRYDVLEANTPBNYFNFVFGGLCGG 300
XX
XX 241 SLVNHPTMCITLAAMVPVNAATVLSLFGVGRYDVLEANTPBNYFNFVFGGLCGG 300
XX 241 SLVNHPTMCITLAAMVPVNAATVLSLFGVGRYDVLEANTPBNYFNFVFGGLCGG 300
XX
XX 301 SRNDYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLKRPVAVADVPLSGFAKADMTLD 360
XX 301 SRNDYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLKRPVAVADVPLSGFAKADMTLD 360
XX
XX 301 SRNDYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLKRPVAVADVPLSGFAKADMTLD 360
XX 301 SRNDYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLKRPVAVADVPLSGFAKADMTLD 360
XX
XX 361 VYLDITGTPLEFVKVNSAINDMGRAVDVYLTQNTSPFPGYNIIVEVNGADQSYMLIE 420
XX 361 VYLDITGTPLEFVKVNSAINDMGRAVDVYLTQNTSPFPGYNIIVEVNGADQSYMLIE 420
XX
XX 361 VYLDITGTPLEFVKVNSAINDMGRAVDVYLTQNTSPFPGYNIIVEVNGADQSYMLIE 420
XX 361 VYLDITGTPLEFVKVNSAINDMGRAVDVYLTQNTSPFPGYNIIVEVNGADQSYMLIE 420
XX
XX 421 NDGAPRTLEPHNHLGHNDYVLGRSPDESASNERHVPFARAGLLSGANPRROVSM 480
XX 421 NDGAPRTLEPHNHLGHNDYVLGRSPDESASNERHVPFARAGLLSGANPRROVSM 480
XX
XX 421 NDGAPRTLEPHNHLGHNDYVLGRSPDESASNERHVPFARAGLLSGANPRROVSE 480
XX 421 NDGAPRTLEPHNHLGHNDYVLGRSPDESASNERHVPFARAGLLSGANPRROVSE 480
XX
XX 481 LPAFGWVLSFRADNPGAWLFHCHIAWHVSGGLGVYLERADDLRGAVSDADADDLRLC 540
XX 481 LPAFGWVLSFRADNPGAWLFHCHIAWHVSGGLGVYLERADDLRGAVSDADADDLRLC 540

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DB 481 LPAFGWVLSFRADNPGAWLFHCHIAWHVSGGLGVYLERADDLRGAVSDADADDLRLC 540
OY 541 ADMRRYPTNPYPKSDSGLKHWRVEGEWLVKA 573
DB 541 ADMRRYPTNPYPKSDSGLKHWRVEGEWLVKA 573

RESULT 14
AAW76316
ID AAW76316 standard; protein; 573 AA.
XX
XX AAW76316;
XX
XX 08-JAN-1999 (first entry)
XX
XX Mycellophthora thermophila laccase protein variant.
XX
XX Laccase; variant; oxidation; dye transfer inhibition; bleaching;
XX denim; lignin modification; paper strengthening; phenol polymerisation;
XX hair dye; waste water treatment.
XX
XX Synthetic.
XX Mycellophthora thermophila.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 106 /label- D106X
XX FT /note- "X is optionally Ala, Val, Pro, Leu, Ile,
XX FT Phe, Tyr or Trp"
XX
XX FT Misc-difference 108 /label- A108X
XX FT /note- "X is optionally Val, Pro, Leu, Ile,
XX FT Phe, Tyr, or Trp"
XX
XX FT Misc-difference 109 /label- N109X
XX FT /note- "X is optionally Ala, Val, Pro, Leu, Ile,
XX FT Phe, Tyr, Gln or Trp"
XX
XX FT Misc-difference 428 /label- T428X
XX FT /note- "X is optionally Ala, Val, Pro, Leu, Ile,
XX FT Phe, Tyr or Trp"
XX
XX FT Misc-difference 500 /label- L500X
XX FT /note- "X is optionally Ile, Phe, Tyr, or Trp"
XX
XX FT Misc-difference 510 /label- S510X
XX FT /note- "X is optionally Ala, Val, Pro, Leu, Ile,
XX FT Phe, Tyr or Trp"
XX
XX FT Misc-difference 511 /label- G511X
XX FT /note- "X is optionally Ala, Val, Pro, Leu, Ile,
XX FT Phe, Tyr or Trp"
XX
XX FT Misc-difference 514 /label- G514X
XX FT /note- "X is optionally Ala, Val, Pro, Leu, Ile,
XX FT Phe, Tyr, or Trp"
XX
XX W09838287-A1.
XX
XX 03-SEP-1998.
XX
XX 23-FEB-1998; 98WO-DK00070.
XX
XX 28-FEB-1997; 97DK-0000222.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Svendsen A, Xu F;
XX
XX WPI; 1998-495393/42.
XX
XX New variants of Coprinus and related laccases with increased

```

Query Match 98.5%; Score 3112; DB 19; Length 573;
Best Local Similarity 98.6%; Pred. No. 1.1e-271;
Matches 565; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 1 QOQSCNTPSNRACWTDGYDINTDYENDSPDTGVVPRPTLTLEVDNMTGPDGVYKEKMYLY 60
DB 1 QOQSCNTPSNRACWTDGYDINTDYENDSPDTGVVPRPTLTLEVDNMTGPDGVYKEKMYLY 60
QY 61 NNSIIGPTIFADMGDTIQYTVINNLETNGTSIMHGLHOKGTNLHDGANGITECPPIPKG 120
DB 61 NNSIIGPTIFADMGDTIQYTVINNLETNGTSIMHGLHOKGTNLHDGANGITECPPIPKG 120
QY 121 GRKVRFEKAOQGTSMVSHSFAOYNGVGAIOINGPASLPYDNDLGVPISDYSSA 180
DB 121 GRKVRFEKAOQGTSMVSHSFAOYNGVGAIOINGPASLPYDNDLGVPISDYSSA 180
QY 181 DELVELTKNSGAPFSDNVLFNCTAKHPEGESEYANVTLPGRHRRLRLINTSVENHFOY 240
DB 181 DELVELTKNSGAPFSDNVLFNCTAKHPEGESEYANVTLPGRHRRLRLINTSVENHFOY 240
QY 241 SLVNHNTMCIIAADMPVNNAMTVDSLELVGQRYDVVIEANRTPGNYMFNVTEGGGLCGG 300
DB 241 SLVNHNTMCIIAADMPVNNAMTVDSLELVGQRYDVVIEANRTPGNYMFNVTEGGGLCGG 300
QY 301 SRNPYPALFHHYAGAPGPGPTDEGKAPVDHNCIDLPNLKPYVAROYPLSGFAKRAADNTLD 360
DB 301 SRNPYPALFHHYAGAPGPGPTDEGKAPVDHNCIDLPNLKPYVAROYPLSGFAKRAADNTLD 360
QY 361 VTLDTTGPFLFVWKVNGSAINIDMGRAVVDYVLTONTSPPGYNIYEVNGADOMSTWLE 420
DB 361 VTLDTTGPFLFVWKVNGSAINIDMGRAVVDYVLTONTSPPGYNIYEVNGADOMSTWLE 420
QY 421 NDPGAPFTLPHPMHLGHDFYVLGRSPDES PASNERHVPDPARADAGLLSGANFRRDYSM 480
DB 421 NDPGAPFTLPHPMHLGHDFYVLGRSPDES PASNERHVPDPARADAGLLSGANFRRDYSM 480
QY 481 LPAFGWVYSEFRADNGAWLFHCHITAMHVSGLGVYTLERADDLRGAVSDADADDLRLC 540
DB 481 LPAFGWVYSEFRADNGAWLFHCHITAMHVSGLGVYTLERADDLRGAVSDADADDLRLC 540
QY 541 ADMRRYWPNTNPKSDSGLKHHRVGEGEWLVKA 573
DB 541 ADMRRYWPNTNPKSDSGLKHHRVGEGEWLVKA 573
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Search completed: December 4, 2002, 10:46:25
Job time : 44 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 10:46:31 ; Search time 17 Seconds

(without alignments)
991.726 Million cell updates/sec

Title: US-09-869-877-10

Perfect score: 3158

Sequence: 1 QOQCNTPSNRACWTDGTDIN.....KSDGLKRWVEGEWLVKA 573

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents.AA.*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/6C.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------|
| 1 | 3158 | 100.0 | 573 | 2 | US-08-991-531-1 |
| 2 | 3158 | 100.0 | 573 | 2 | US-09-032-315-10 |
| 3 | 3158 | 100.0 | 573 | 2 | US-08-993-318A-10 |
| 4 | 3158 | 100.0 | 573 | 3 | US-09-028-887-1 |
| 5 | 3158 | 100.0 | 573 | 4 | US-09-399-886-10 |
| 6 | 3158 | 100.0 | 573 | 4 | US-09-396-260-10 |
| 7 | 3158 | 100.0 | 573 | 4 | US-09-518-901-1 |
| 8 | 3158 | 100.0 | 573 | 4 | US-09-576-281-10 |
| 9 | 3158 | 100.0 | 620 | 1 | US-08-706-037-27 |
| 10 | 3158 | 100.0 | 620 | 2 | US-09-005-337-27 |
| 11 | 3158 | 100.0 | 620 | 5 | PCT-US95-06815-2 |
| 12 | 3158 | 100.0 | 620 | 1 | US-08-940-661A-2 |
| 13 | 3127 | 99.0 | 620 | 2 | US-09-083-485-2 |
| 14 | 3127 | 99.0 | 620 | 2 | US-08-939-218A-2 |
| 15 | 2089.5 | 66.2 | 616 | 1 | US-08-749-882A-2 |
| 16 | 2089.5 | 66.2 | 616 | 2 | US-08-539-114-2 |
| 17 | 2084.5 | 66.0 | 616 | 5 | PCT-US95-06816-2 |
| 18 | 2076.5 | 65.8 | 616 | 2 | US-08-991-531-2 |
| 19 | 2076.5 | 65.8 | 616 | 2 | US-09-032-315-9 |
| 20 | 2076.5 | 65.8 | 616 | 3 | US-08-993-318A-9 |
| 21 | 2076.5 | 65.8 | 616 | 4 | US-09-028-887-2 |
| 22 | 2076.5 | 65.8 | 616 | 4 | US-09-399-886-9 |
| 23 | 2076.5 | 65.8 | 616 | 4 | US-09-396-260-9 |
| 24 | 2076.5 | 65.8 | 616 | 4 | US-09-518-901-2 |
| 25 | 2076.5 | 65.8 | 616 | 4 | US-09-576-281-9 |
| 26 | 636 | 20.1 | 499 | 2 | US-09-032-315-2 |
| 27 | 636 | 20.1 | 499 | 2 | US-08-993-318A-2 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|--------------------|
| 28 | 636 | 20.1 | 499 | 4 | US-09-399-886-2 | Sequence 2, Appli |
| 29 | 636 | 20.1 | 499 | 4 | US-09-396-260-2 | Sequence 2, Appli |
| 30 | 636 | 20.1 | 499 | 4 | US-09-576-281-2 | Sequence 2, Appli |
| 31 | 636 | 20.1 | 520 | 1 | US-08-462-484-2 | Sequence 2, Appli |
| 32 | 636 | 20.1 | 520 | 1 | US-08-441-147-2 | Sequence 2, Appli |
| 33 | 636 | 20.1 | 520 | 5 | PCT-US95-07536-2 | Sequence 2, Appli |
| 34 | 614 | 19.4 | 539 | 2 | US-09-032-315-1 | Sequence 1, Appli |
| 35 | 614 | 19.4 | 539 | 3 | US-08-689-421-27 | Sequence 1, Appli |
| 36 | 614 | 19.4 | 539 | 4 | US-08-993-318A-1 | Sequence 27, Appli |
| 37 | 614 | 19.4 | 539 | 4 | US-09-396-260-1 | Sequence 1, Appli |
| 38 | 614 | 19.4 | 539 | 4 | US-09-396-260-1 | Sequence 1, Appli |
| 39 | 614 | 19.4 | 539 | 4 | US-09-389-528-27 | Sequence 27, Appli |
| 40 | 614 | 19.4 | 539 | 4 | US-09-181-827A-27 | Sequence 27, Appli |
| 41 | 614 | 19.4 | 539 | 4 | US-09-576-281-1 | Sequence 1, Appli |
| 42 | 609.5 | 19.3 | 529 | 1 | US-08-172-331B-14 | Sequence 14, Appli |
| 43 | 609.5 | 19.3 | 529 | 1 | US-08-706-037-25 | Sequence 25, Appli |
| 44 | 609.5 | 19.3 | 529 | 2 | US-09-005-337-25 | Sequence 25, Appli |
| 45 | 609.5 | 19.3 | 529 | 2 | US-09-032-315-5 | Sequence 5, Appli |

ALIGNMENTS

RESULT 1
US-08-991-531-1
Sequence 1, Application US/08991531
Patent No. 5925554
GENERAL INFORMATION:
APPLICANT: Pedersen, Anders Hjelholt
APPLICANT: Svendsen, Allan
APPLICANT: Schneider, Palle
APPLICANT: Rasmussen, Grethe
APPLICANT: Cherry, Joel
TITLE OF INVENTION: Myceliophthora And scytailidium laccase
TITLE OF SEQUENCES: Variants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESS: No. 59255540 No. 5925554disk of No. 5925554th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,531
FILING DATE: 16-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5125, 200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-991-531-1

Query Match 100.0%; Score 3158; DB 2; Length 573;
Best Local Similarity 100.0%; Pred. No. 3.6e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QOQCNTPSNRACWTDGTDINTDYEVDSPDTGVVRYTTLTEVDNMWGTGPDGVYKRVMLV 60

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,318A
FILING DATE: December 18, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-318A-10

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Query Match      100.0%; Score 3158; DB 2; Length 573;
Best Local Similarity 100.0%; Pred. No. 3.6e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QOSCTPSNRACWTGDTGDTINTDYENDSPDTGVRRPYTLTLEVDNMTGPDGVYKEKMYLV 60
DB 1 QOSCTPSNRACWTGDTGDTINTDYENDSPDTGVRRPYTLTLEVDNMTGPDGVYKEKMYLV 60
QY 61 NNSIIGPTIFADMGDTIOYVINNLETNGTSIHHMGLHOKGTNLHDGANGITECPPIPKG 120
DB 61 NNSIIGPTIFADMGDTIOYVINNLETNGTSIHHMGLHOKGTNLHDGANGITECPPIPKG 120
QY 121 GKKVYRFAKQOYGTSMYHSHFSAQYNGVGAQIINGPASLPYDTDLGVPPISDYSSA 180
DB 121 GKKVYRFAKQOYGTSMYHSHFSAQYNGVGAQIINGPASLPYDTDLGVPPISDYSSA 180
QY 181 DELVELITKNSGAPFSDNVLENGTAKHPEETGEGETANYTLTPGRRHRLRLINTSVENHFOY 240
DB 181 DELVELITKNSGAPFSDNVLENGTAKHPEETGEGETANYTLTPGRRHRLRLINTSVENHFOY 240
QY 241 SLVNHHTMCIIAADMPVNAATVDSLFLGVGORYDVVIEANRTPGNYFNVTGGGLLCGG 300
DB 241 SLVNHHTMCIIAADMPVNAATVDSLFLGVGORYDVVIEANRTPGNYFNVTGGGLLCGG 300
QY 301 SRNPYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVADVPLSGFAKRAADNTLD 360
DB 301 SRNPYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVADVPLSGFAKRAADNTLD 360
QY 361 VILDTTGTPLFLFWKVGSAINIDMGRAVVDYVLTQNTSFPFGNYIVVNGADQMSYMLIE 420
DB 361 VILDTTGTPLFLFWKVGSAINIDMGRAVVDYVLTQNTSFPFGNYIVVNGADQMSYMLIE 420
QY 421 NDPGAPFTLPHPMHLGHDFYVLGRSPDESPASNERHVPFPDADAGLLSGANPYRQVSM 480
DB 421 NDPGAPFTLPHPMHLGHDFYVLGRSPDESPASNERHVPFPDADAGLLSGANPYRQVSM 480
QY 481 LPAFGWVLSFRADNPGAMLFCHIAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
DB 481 LPAFGWVLSFRADNPGAMLFCHIAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
QY 541 ADMRRYWPNTNPPKSDSGLKHRRVGEEMLVKA 573
DB 541 ADMRRYWPNTNPPKSDSGLKHRRVGEEMLVKA 573

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RESULT 4
US-09-028-887-1
; Sequence 1, Application us/09028887
; Patent No. 6060442

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```

GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6060442o No. 6060442disk of No. 6060442th America
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,887
FILING DATE: 24-February-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 5201.200-US
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-028-887-1

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Query Match      100.0%; Score 3158; DB 3; Length 573;
Best Local Similarity 100.0%; Pred. No. 3.6e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QOSCTPSNRACWTGDTGDTINTDYENDSPDTGVRRPYTLTLEVDNMTGPDGVYKEKMYLV 60
DB 1 QOSCTPSNRACWTGDTGDTINTDYENDSPDTGVRRPYTLTLEVDNMTGPDGVYKEKMYLV 60
QY 61 NNSIIGPTIFADMGDTIOYVINNLETNGTSIHHMGLHOKGTNLHDGANGITECPPIPKG 120
DB 61 NNSIIGPTIFADMGDTIOYVINNLETNGTSIHHMGLHOKGTNLHDGANGITECPPIPKG 120
QY 121 GKKVYRFAKQOYGTSMYHSHFSAQYNGVGAQIINGPASLPYDTDLGVPPISDYSSA 180
DB 121 GKKVYRFAKQOYGTSMYHSHFSAQYNGVGAQIINGPASLPYDTDLGVPPISDYSSA 180
QY 181 DELVELITKNSGAPFSDNVLENGTAKHPEETGEGETANYTLTPGRRHRLRLINTSVENHFOY 240
DB 181 DELVELITKNSGAPFSDNVLENGTAKHPEETGEGETANYTLTPGRRHRLRLINTSVENHFOY 240
QY 241 SLVNHHTMCIIAADMPVNAATVDSLFLGVGORYDVVIEANRTPGNYFNVTGGGLLCGG 300
DB 241 SLVNHHTMCIIAADMPVNAATVDSLFLGVGORYDVVIEANRTPGNYFNVTGGGLLCGG 300
QY 301 SRNPYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVADVPLSGFAKRAADNTLD 360
DB 301 SRNPYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVADVPLSGFAKRAADNTLD 360
QY 361 VILDTTGTPLFLFWKVGSAINIDMGRAVVDYVLTQNTSFPFGNYIVVNGADQMSYMLIE 420
DB 361 VILDTTGTPLFLFWKVGSAINIDMGRAVVDYVLTQNTSFPFGNYIVVNGADQMSYMLIE 420
QY 421 NDPGAPFTLPHPMHLGHDFYVLGRSPDESPASNERHVPFPDADAGLLSGANPYRQVSM 480
DB 421 NDPGAPFTLPHPMHLGHDFYVLGRSPDESPASNERHVPFPDADAGLLSGANPYRQVSM 480
QY 481 LPAFGWVLSFRADNPGAMLFCHIAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
DB 481 LPAFGWVLSFRADNPGAMLFCHIAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540

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1 QOOSCTPSNRACWTGDIINTDIEVDSPDGVRRPTLTLLTEVDNMTGPDGVYKEKVMY 60
61 NNSIIGPTIFADMGDTIOYVIVNNLETNGTSHMHGJHOKGTMLHDGANGITECP1PPKG 120
61 NNSIIGPTIFADMGDTIOYVIVNNLETNGTSHMHGJHOKGTMLHDGANGITECP1PPKG 120
121 GKRVRFKAQOYGTSMYHSHFSAQYNGVYGAIOINGPASLPYDTDLGVFPISDYSSA 180
121 GKRVRFKAQOYGTSMYHSHFSAQYNGVYGAIOINGPASLPYDTDLGVFPISDYSSA 180
181 DELVELTKNSGAFSDNVLFNGTAKHPEEGEYANVTLPGRHRRLRLINTSVENHFOY 240
181 DELVELTKNSGAFSDNVLFNGTAKHPEEGEYANVTLPGRHRRLRLINTSVENHFOY 240
241 SLVNHMTCTIADMVVNMTVDLSFLVGQORYDVYIEANRPTGNWNTFEGGILLCG 300
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301 SRNPYPAAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVARADVPLSGFAKADNTLD 360
301 SRNPYPAAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVARADVPLSGFAKADNTLD 360
361 VTLDTTGTPLFWKVGSAINIDMGRAVVDYVLTONTSPPGNIYEVGADQMSYTWLE 420
361 VTLDTTGTPLFWKVGSAINIDMGRAVVDYVLTONTSPPGNIYEVGADQMSYTWLE 420
421 NDGPAPFTLPHPMHLHGHPYVYLGSRPDESPASNERHVPDPADAGLLSGANVRDYVM 480
421 NDGPAPFTLPHPMHLHGHPYVYLGSRPDESPASNERHVPDPADAGLLSGANVRDYVM 480
481 LPAFGWVLSFRADNPGAMLFHCHIAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
481 LPAFGWVLSFRADNPGAMLFHCHIAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
541 ADMRRYPTNPYPKSDSGLKHRRVEEGEWLVKA 573
541 ADMRRYPTNPYPKSDSGLKHRRVEEGEWLVKA 573

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RESULT 7
 US-09-518-901-1
 ; Sequence 1, Application US/09518901
 ; Patent No. 6218170
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; TITLE OF INVENTION: LACCASE MUTANTS
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 62181700 No. 6218170disk of No. 6218170th America
 ; STREET: 405 Lexington Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10174
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/518, 901
 ; FILING DATE: 06-Mar-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/028, 887
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gregg, Valeta A.
 ; REGISTRATION NUMBER: 35,127
 ; REFERENCE/DOCKET NUMBER: 5201.200-US
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:

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; LENGTH: 573 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-518-901-1
Query Match 100.0%; Score 3158; DB 4; Length 573;
Best Local Similarity 100.0%; Pred. No. 3.6e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 QOOSCTPSNRACWTGDIINTDIEVDSPDGVRRPTLTLLTEVDNMTGPDGVYKEKVMY 60
1 NNSIIGPTIFADMGDTIOYVIVNNLETNGTSHMHGJHOKGTMLHDGANGITECP1PPKG 120
61 NNSIIGPTIFADMGDTIOYVIVNNLETNGTSHMHGJHOKGTMLHDGANGITECP1PPKG 120
121 GKRVRFKAQOYGTSMYHSHFSAQYNGVYGAIOINGPASLPYDTDLGVFPISDYSSA 180
121 GKRVRFKAQOYGTSMYHSHFSAQYNGVYGAIOINGPASLPYDTDLGVFPISDYSSA 180
181 DELVELTKNSGAFSDNVLFNGTAKHPEEGEYANVTLPGRHRRLRLINTSVENHFOY 240
181 DELVELTKNSGAFSDNVLFNGTAKHPEEGEYANVTLPGRHRRLRLINTSVENHFOY 240
241 SLVNHMTCTIADMVVNMTVDLSFLVGQORYDVYIEANRPTGNWNTFEGGILLCG 300
241 SLVNHMTCTIADMVVNMTVDLSFLVGQORYDVYIEANRPTGNWNTFEGGILLCG 300
301 SRNPYPAAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVARADVPLSGFAKADNTLD 360
301 SRNPYPAAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVARADVPLSGFAKADNTLD 360
361 VTLDTTGTPLFWKVGSAINIDMGRAVVDYVLTONTSPPGNIYEVGADQMSYTWLE 420
361 VTLDTTGTPLFWKVGSAINIDMGRAVVDYVLTONTSPPGNIYEVGADQMSYTWLE 420
421 NDGPAPFTLPHPMHLHGHPYVYLGSRPDESPASNERHVPDPADAGLLSGANVRDYVM 480
421 NDGPAPFTLPHPMHLHGHPYVYLGSRPDESPASNERHVPDPADAGLLSGANVRDYVM 480
481 LPAFGWVLSFRADNPGAMLFHCHIAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
481 LPAFGWVLSFRADNPGAMLFHCHIAMHVSGLGVYLLERADDLRGAVSDADADDLRLC 540
541 ADMRRYPTNPYPKSDSGLKHRRVEEGEWLVKA 573
541 ADMRRYPTNPYPKSDSGLKHRRVEEGEWLVKA 573

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RESULT 8
 US-09-576-281-10
 ; Sequence 10, Application US/09576281
 ; Patent No. 6277611
 ; GENERAL INFORMATION:
 ; APPLICANT: Pedersen, Anders
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Schneider, Palle
 ; APPLICANT: Rasmussen, Grethe
 ; APPLICANT: Cherry, Joel
 ; TITLE OF INVENTION: LACCASE MUTANTS
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 62776110 No. 6277611disk of No. 6277611th America
 ; STREET: 405 Lexington Avenue
 ; CITY: New York
 ; COUNTRY: USA
 ; ZIP: 10174
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

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Db 408 VILDTGTPLFWKVGSAINIDMGRAVVDYLTQNTSPPGYNIIVEVNGADQMSYWLIE 467
Qy 421 NDGAPFTLPHPMHLGHDFYVYGRSPDESPASNERHVEDPADACILSGANFVRDYSM 480
Db 468 NDGAPFTLPHPMHLGHDFYVYGRSPDESPASNERHVEDPADACILSGANFVRDYSM 527
Qy 481 LPAFGVVLSPFADNPGANLFFCHIAMHVSGLGVYTLERADLRGAVSDADADLDRLC 540
Db 528 LPAFGVVLSPFADNPGANLFFCHIAMHVSGLGVYTLERADLRGAVSDADADLDRLC 587
Qy 541 ADMRRYPTNPYPKSDSGLKHRRVVEGEWLKKA 573
Db 588 ADMRRYPTNPYPKSDSGLKHRRVVEGEWLKKA 620

RESULT 10
US-09-005-397-27
; Sequence 27, Application US/09005397
; Patent No. 5972670
; GENERAL INFORMATION:
; APPLICANT: Xu, Feng
; APPLICANT: Berka, Randy M.
; APPLICANT: Mahleithner, Jill A.
; TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH
; TITLE OF INVENTION: ENHANCED ACTIVITY
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59726700 No. 5972670disk of No. 5972670th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/706,037
; FILING DATE: 30-AUG-1996
; APPLICATION NUMBER: US 60/002,800
; FILING DATE: 1-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4526, 200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-005-397-27

Query Match 100.0%; Score 3158; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 4e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSCTPSNRACMTDGYDINDYEDSPDGVVRYTLFLFVNDWMTGPDGVYKKKVMY 60
Db 48 QOSCTPSNRACMTDGYDINDYEDSPDGVVRYTLFLFVNDWMTGPDGVYKKKVMY 107
Qy 61 NSIIGPTIFADMGDTIQVTVINLETNGTSHHGLHOKGTNLHDGANGIIECPPIPKG 120
|||||

Db 108 NSIIGPTIFADMGDTIQVTVINLETNGTSHHGLHOKGTNLHDGANGIIECPPIPKG 167
Qy 121 GRKYRFFKAQOYCTSWYHSHFSAOYGNVGAIOINGPASTLPYDTDLGVPIISDYSSA 180
Db 168 GRKYRFFKAQOYCTSWYHSHFSAOYGNVGAIOINGPASTLPYDTDLGVPIISDYSSA 227
Qy 181 DELVELTKNSGAFESDNVLENGTAKHPEEGEYANVTLPGRHRLRLINTSVENHFOY 240
Db 228 DELVELTKNSGAFESDNVLENGTAKHPEEGEYANVTLPGRHRLRLINTSVENHFOY 287
Qy 241 SLVNHMCTIADMPVNMATVDSLFLVGQRVDVYTEANRTGNTWENTFEGGLCG 300
Db 288 SLVNHMCTIADMPVNMATVDSLFLVGQRVDVYTEANRTGNTWENTFEGGLCG 347
Qy 301 SRNPYPALFHYAGAPGPTDEGKAPVBNCDLPLEKPVVARDVPLSGFARADNTLD 360
Db 348 SRNPYPALFHYAGAPGPTDEGKAPVBNCDLPLEKPVVARDVPLSGFARADNTLD 407
Qy 361 VILDTGTPLFWKVGSAINIDMGRAVVDYLTQNTSPPGYNIIVEVNGADQMSYWLIE 420
Db 408 VILDTGTPLFWKVGSAINIDMGRAVVDYLTQNTSPPGYNIIVEVNGADQMSYWLIE 467
Qy 421 NDGAPFTLPHPMHLGHDFYVYGRSPDESPASNERHVEDPADACILSGANFVRDYSM 480
Db 468 NDGAPFTLPHPMHLGHDFYVYGRSPDESPASNERHVEDPADACILSGANFVRDYSM 527
Qy 481 LPAFGVVLSPFADNPGANLFFCHIAMHVSGLGVYTLERADLRGAVSDADADLDRLC 540
Db 528 LPAFGVVLSPFADNPGANLFFCHIAMHVSGLGVYTLERADLRGAVSDADADLDRLC 587
Qy 541 ADMRRYPTNPYPKSDSGLKHRRVVEGEWLKKA 573
Db 588 ADMRRYPTNPYPKSDSGLKHRRVVEGEWLKKA 620

RESULT 11
PCT-US95-06815-2
; Sequence 2, Application PC/TUS9506815
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PURIFIED MYCELIOPTHORA LACCASES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06815
; FILING DATE: 31-May-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/253,781
; FILING DATE: 03-June-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowmey, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4184, 204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

Sequence 2, Application US/09083485
Patent No. 5948121
GENERAL INFORMATION:
APPLICANT: Dorrit Aaslyng
APPLICANT: Sorensen, Niels H.
TITLE OF INVENTION: Laccases with Improved Dyeing
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 5948121 of No. 5948121 of No. 5948121 of America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,485
FILING DATE: 20-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4639, 204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-083-485-2

Query Match 99.0%; Score 3127; DB 2; Length 620;
Best Local Similarity 99.0%; Pred. No. 3.5e-287;
Matches 567; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QOSNTSPNRACWTDGDIINTDYEVSDPGVVRPTLTLEVDNMTGPDGVVEKWL 60
DB 48 QOSNTSPNRACWTDGDIINTDYEVSDPGVVRPTLTLEVDNMTGPDGVVEKWL 107
QY 61 NNSIIGPTIFADMGDTIQVYINNLETNGTSHHGHGLOKGTNLHDGANGTECPPIPKG 120
DB 108 NNSIIGPTIFADMGDTIQVYINNLETNGTSHHGHGLOKGTNLHDGANGTECPPIPKG 167
QY 121 GRKYRFRKAQOYGTSMYSHESAQYGNVGVAIQINGPASPYPDTDLGVFPISDYSSA 180
DB 168 GRKYRFRKAQOYGTSMYSHESAQYGNVGVAIQINGPASPYPDTDLGVFPISDYSSA 227
QY 181 DELVELTKNSGAPSDVNLFGTAKHPTGEGEYANVTLTGRRRLRLITSVENHFOV 240
DB 228 DELVELTKNSGAPSDVNLFGTAKHPTGEGEYANVTLTGRRRLRLITSVENHFOV 287
QY 241 SLVNHWTACIIAADVVPVNAATVDSLFLGVGORYDVIEANRTPGNYMENVTEGGGLCG 300
DB 288 SLVNHWTACIIAADVVPVNAATVDSLFLGVGORYDVIEANRTPGNYMENVTEGGGLCG 347
QY 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVARDVPLSGFAKRADNTLD 360
DB 348 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVARDVPLSGFAKRADNTLD 407
QY 361 VTLDGTSTPLFVWKVNSAINIIDGRAVVDVLTQNTSEFPGYNIYEVNGADOMSYWLE 420
DB 408 VTLDGTSTPLFVWKVNSAINIIDGRAVVDVLTQNTSEFPGYNIYEVNGADOMSYWLE 467
QY 421 NDBGAPFTLPHPMHLHGHDFVILGRSPDESPASNERHVFDPARDAGLLGSANPVRDVS 480
DB 468 NDBGAPFTLPHPMHLHGHDFVILGRSPDESPASNERHVFDPARDAGLLGSANPVRDVS 527

QY 481 LPARGWVILSEFADNPGAMLEFRCHIAHVSGLGVYLERADDLRGAVSDADADDLRLC 540
DB 528 LPARGWVILSEFADNPGAMLEFRCHIAHVSGLGVYLERADDLRGAVSDADADDLRLC 587
QY 541 ADMRRYPTNTPKSDSGLKIRWVEEGEWLVKA 573
DB 568 ADMRRYPTNTPKSDSGLKIRWVEEGEWLVKA 620

RESULT 14
US-08-939-218A-2
Sequence 2, Application US/08939218A
Patent No. 5981243
GENERAL INFORMATION:
APPLICANT: BERKA, Randy Michael
APPLICANT: BROWN, Stephen H.
APPLICANT: XU, Peng
APPLICANT: SCHNEIDER, Palle
APPLICANT: OXENB LL, Karen M.
TITLE OF INVENTION: PURIFIED MYCELIOPHYTHORA LACCASES AND NUCLEIC
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 5981243 of No. 5981243 of No. 5981243 of America, Inc.
STREET: 405 Lexington Avenue, 64th floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,218A
FILING DATE: 29-SEPT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol E.
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 4184, 120-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-939-218A-2

Query Match 99.0%; Score 3127; DB 2; Length 620;
Best Local Similarity 99.0%; Pred. No. 3.5e-287;
Matches 567; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QOSNTSPNRACWTDGDIINTDYEVSDPGVVRPTLTLEVDNMTGPDGVVEKWL 60
DB 48 QOSNTSPNRACWTDGDIINTDYEVSDPGVVRPTLTLEVDNMTGPDGVVEKWL 107
QY 61 NNSIIGPTIFADMGDTIQVYINNLETNGTSHHGHGLOKGTNLHDGANGTECPPIPKG 120
DB 108 NNSIIGPTIFADMGDTIQVYINNLETNGTSHHGHGLOKGTNLHDGANGTECPPIPKG 167
QY 121 GRKYRFRKAQOYGTSMYSHESAQYGNVGVAIQINGPASPYPDTDLGVFPISDYSSA 180
DB 168 GRKYRFRKAQOYGTSMYSHESAQYGNVGVAIQINGPASPYPDTDLGVFPISDYSSA 227
QY 181 DELVELTKNSGAPSDVNLFGTAKHPTGEGEYANVTLTGRRRLRLITSVENHFOV 240

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 10:47:46 ; Search time 12 Seconds

(without alignments)
775.570 Million cell updates/sec

Title: US-09-869-877-10

Perfect score: 3158

Sequence: 1 QOCSNTPSNRACWTDGYDIN.....KSDSGIKHWEVGEMLYKA 573

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues 103943

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications RA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB pep:*
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- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB pep:*
- 10: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB pep:*
- 11: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB pep:*
- 12: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB pep:*
- 13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB pep:*
- 14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|------------------------------------|
| 1 | 3158 | 100.0 | 573 | 10 | US-09-732-350-10 Sequence 10, Appl |
| 2 | 2076.5 | 65.8 | 616 | 10 | US-09-732-350-9 Sequence 9, Appl |
| 3 | 636 | 20.1 | 499 | 10 | US-09-732-350-2 Sequence 2, Appl |
| 4 | 614 | 19.4 | 539 | 10 | US-09-732-350-1 Sequence 1, Appl |
| 5 | 609.5 | 19.3 | 529 | 10 | US-09-732-350-5 Sequence 5, Appl |
| 6 | 571 | 18.1 | 499 | 10 | US-09-732-350-3 Sequence 3, Appl |
| 7 | 565 | 17.9 | 572 | 10 | US-09-732-350-7 Sequence 7, Appl |
| 8 | 557.5 | 17.7 | 575 | 10 | US-09-732-350-8 Sequence 8, Appl |
| 9 | 556 | 17.6 | 548 | 10 | US-09-732-350-4 Sequence 4, Appl |
| 10 | 542 | 17.2 | 599 | 10 | US-09-732-350-6 Sequence 6, Appl |
| 11 | 446 | 14.1 | 564 | 9 | US-09-944-160-12 Sequence 12, Appl |
| 12 | 241 | 7.6 | 583 | 9 | US-09-942-185-2 Sequence 2, Appl |
| 13 | 204 | 6.5 | 572 | 9 | US-09-942-185-4 Sequence 4, Appl |
| 14 | 198 | 6.3 | 568 | 12 | US-10-080-233-4 Sequence 4, Appl |
| 15 | 197 | 6.2 | 594 | 10 | US-09-338-723A-2 Sequence 2, Appl |
| 16 | 197 | 6.2 | 594 | 12 | US-10-080-210-2 Sequence 2, Appl |
| 17 | 197 | 6.2 | 594 | 10 | US-10-080-233-2 Sequence 2, Appl |
| 18 | 195.5 | 6.2 | 627 | 10 | US-09-338-723A-4 Sequence 4, Appl |
| 19 | 195.5 | 6.2 | 627 | 12 | US-10-080-210-4 Sequence 4, Appl |

| | | | | | |
|----|-------|-----|------|----|---------------------------------------|
| 20 | 195.5 | 6.2 | 627 | 12 | US-10-080-210-7 Sequence 7, Appl |
| 21 | 120.5 | 3.8 | 545 | 10 | US-09-988-200-8 Sequence 8, Appl |
| 22 | 101.5 | 3.2 | 1016 | 12 | US-10-007-693-95 Sequence 95, Appl |
| 23 | 101 | 3.2 | 1260 | 9 | US-10-024-918-27 Sequence 27, Appl |
| 24 | 101 | 3.2 | 1477 | 9 | US-10-092-880-4 Sequence 4, Appl |
| 25 | 99 | 3.1 | 404 | 10 | US-09-815-242-11242 Sequence 11242, A |
| 26 | 98 | 3.1 | 522 | 12 | US-10-090-624-4 Sequence 4, Appl |
| 27 | 97 | 3.1 | 821 | 9 | US-09-764-868-883 Sequence 883, App |
| 28 | 96.5 | 3.1 | 485 | 9 | US-09-918-543-2 Sequence 2, Appl |
| 29 | 96.5 | 3.1 | 485 | 10 | US-09-769-864-1 Sequence 7, Appl |
| 30 | 96.5 | 3.1 | 485 | 10 | US-09-854-346-2 Sequence 2, Appl |
| 31 | 96.5 | 3.1 | 485 | 10 | US-09-902-188A-1 Sequence 1, Appl |
| 32 | 96.5 | 3.1 | 485 | 10 | US-09-833-435A-3 Sequence 3, Appl |
| 33 | 96.5 | 3.1 | 726 | 10 | US-09-833-435A-13 Sequence 13, Appl |
| 34 | 96.5 | 3.1 | 726 | 10 | US-09-871-212-8 Sequence 8, Appl |
| 35 | 96 | 3.0 | 448 | 10 | US-09-841-132-445 Sequence 445, App |
| 36 | 96 | 3.0 | 1751 | 10 | US-09-841-132-594 Sequence 594, App |
| 37 | 96 | 3.0 | 1751 | 10 | US-09-841-132-594 Sequence 16, App |
| 38 | 95 | 3.0 | 654 | 12 | US-10-090-624-16 Sequence 425, App |
| 39 | 95 | 3.0 | 1184 | 9 | US-09-978-697-425 Sequence 425, App |
| 40 | 95 | 3.0 | 1184 | 9 | US-09-978-697-425 Sequence 4, Appl |
| 41 | 95 | 3.0 | 1184 | 9 | US-09-978-697-425 Sequence 11963, A |
| 42 | 94.5 | 3.0 | 776 | 10 | US-09-833-435A-4 Sequence 4, Appl |
| 43 | 93.5 | 3.0 | 1261 | 10 | US-09-815-242-11963 Sequence 6, Appl |
| 44 | 93 | 2.9 | 867 | 9 | US-09-839-894-6 Sequence 32, Appl |
| 45 | 93 | 2.9 | 881 | 10 | US-09-850-351A-32 |

ALIGNMENTS

RESULT 1
US-09-732-350-10
Sequence 10, Application US/09732350
Patient No. US20010031490A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Xu, Feng
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20010031490A10 No. US20010031490A1disk of No. US20010031490A1
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732.350
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/032,315
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

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ADDRESSSEE: NO. US20010031490A10 No. US20010031490A1disk of No. US20010031490A1th
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732.350
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/032.315
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-732-350-2

Query Match 20.1%; Score 636; DB 10; Length 499;
Best Local Similarity 33.0%; Pred. No. 1.9e-46;
Matches 184; Conservative 69; Mismatches 204; Indels 100; Gaps 24;

QY 31 GVVREPTLTLEVDNMTGPDGVYKREKVMVNNSTIGPTIFADMGDTIQVTVNNLETN-- 88
DB 3 GPVADLTITNAV-----SPDGSRQAV-VVNGTFRGLITGNMGDRFQVNTVDNLTNHTM 57
QY 89 --GTSIHNGHGHOKTNLHDGANGITECPTRPKGGRKYRFRK-QOYGSWYSHSAY 145
DB 58 LKSTSIHNGHGFQKGTNADGAFINQCP1-SSGHSFLDFQVDDAGTFWVHSHLSY 116
QY 146 GNGVVAIQI---NGPASIPTYDILG--VFPISDIYSSADELVELTKNSGAPF---SDN 197
DB 117 CDGLNGRPVYVDPNDPAADLVYDNDQVITYLVDTKHYAA-----KLGPAFPLGADA 168
QY 198 VLENGTAKHPETGECEYANVTLPGRRRRLRLINTSVENHFOVSLVNHHTMCITIAADVPV 257
DB 169 TLINKGSPSTTTADLSVTPGKRYRFLVSLSCDPNMFSSIDGHNMTIETDSINT 228
QY 258 NAMVYDSLELGORYDYVTEANKRPENWTF--NTFFGGGLCGGSRNTPPAIFHYAGA 315
DB 229 APLVYDSIOIFAQRYSFVLEANOAVDNYMIRANPNFNGVGTGGIN---SAILKYDGA 284
QY 316 PGCPPT---DEGKAPVDNHCIDLPNLKPYVARDVPLSGFAKRAVDNLTDTGTPLFV 372
DB 285 AAVERTTTQTTSTAP-----LNEVNLHPLVTTAVPSPAGVADLAINNAFENNGINFF- 338
QY 373 WKVNGSAINIIDGRAVVDVYL-TQNTS--FPPG--YNIIVEANGADQSWYLLIENDGAPF 427
DB 339 --INASFPPTVPVPLQITISGQNNQDILLPSGSVYSLDS-NADTIFSPATAAGCA-- 393
QY 428 TLPHNMLHGHFTYVIGRSPDESASNEKRVPEPADAG--LLSGANPVYRQV--SMRPA 463
DB 394 --PHFPHLGHAFAYV-----RSAGSTVYVNDNPJFRDVSSTGTPA 432
QY 484 FG-WVYLSFRANPGAMLFHCHTAMVHVSGLGVYLERADRLGAVSADADADLRLCAD 542
DB 433 ACDNVTIRRTDNPGWFLHCHIDFULEAGFAVVEADITDVASA----- 477

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QY 543 WRRTWPTNPKRSDSGL 559
DB 478 -----NPVPOAWSDL 487

RESULT 4
US-09-732-350-1
Sequence 1, Application US/09732350
Patent No. US20010031490A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Xu, Feng
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSSEE: NO. US20010031490A10 No. US20010031490A1disk of No. US20010031490A1
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732.350
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/032.315
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-732-350-1

Query Match 19.4%; Score 614; DB 10; Length 539;
Best Local Similarity 32.5%; Pred. No. 1.6e-44;
Matches 174; Conservative 70; Mismatches 204; Indels 88; Gaps 21;

QY 37 TLITFEVDNMTGPDGVYKREKVMVNNSTIGPTIFADMGDTIQVTVNNLETN--NGTSI 92
DB 26 TMLTITNAN--VSPDGTFRGLIV--NGVHPLRIGKRNDFELANVDNDNPLMRPTSI 81
QY 93 HHNGHGHOKTNLHDGANGITECPTRPKGGRKYRFR-KAOYGSWYSHSAYGNGVVG 151
DB 82 HHNGHGHOKTNLHDGANGITECPTRPKGGRKYRFR-KAOYGSWYSHSAYGNGVVG 140
QY 152 AIOI---NGPASIPTYDILG--VFPISDIYSSADELVELTKNSGAPFSDNVLFNCTAH 206
DB 141 PMVITYDNDPNAHALYDEDEENTITLADWYHHPAPSI-----QGAAPDPAITLNGKGR 194
QY 207 PEGGECEYANVTLPGRRRRLRLINTSVENHFOVSLVNHHTMCITIAADVPVNAITVDSLF 266
DB 195 VGGPAAELSTVNEQGRKTRMLRLISLSCDPNMFSSIDGHELTITLVDGGLTEPHTDRQ 254
QY 267 LGVGRYDYVTEANKRPENWTF--TFGGGLCGGSRNTPPAIFHYAGAPGPPYDGG 324
DB 255 IFTGORYSFVLANQVVDNYMIRANPNKGRNGLAGTFANGVNSAILRYAGANADPTTSA 314

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QY 273 YDVIEANTPGNWNWTFEGGGLG--GSRNPYPAIFHYAGAP-GGPTDEKAPVD 329
 DB 266 YSFILADQDVONMYIRAMPAGIGITTFAGGIN---SALIRDGADVETTTQATSPV- 321
 QY 330 HNCIDLPLKPVVADVPLSGFAKRAADNTLDVTTGTPLEFWKVSAINIDMGRAVV 389
 DB 322 -VLSSESNIAPLTNAAPGLPEVGGVDLAINFNLFEDG-PSLKFQINGV----- 367
 QY 390 DYVLQNTSPFGYNYV--EVNGADQMS-----YMLIEND-----PGAPFTLPHM 433
 DB 368 -----TEFPTVTVLQILISGAGSADLLPSGVYALPSPNTIELSLPAGALGGPHF 420
 QY 434 HLHGDFYVIGRSPDESASNERHVEDPARDAGLLSGANPRVDYSLMPLAFG-WVYLSR 492
 DB 421 HLHGTFSVV-----RPAGSTTYN-----VAPGQDVYSGNTGDNVIRRD 463
 QY 493 ADNPGAMLEFHCHIAHVSGGLGVYLERADLR 525
 DB 464 TNNPGMFLHCHIDMHLLEAMLPISLRTSLTLR 496

RESULT 10

US-09-732-350-6
 ; Sequence 6, Application US/09732350
 ; Patent No. US20010031490A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Xu, Peng
 ; TITLE OF INVENTION: LACCASE MUTANTS
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. US20010031490A10 No. US20010031490A1disk of No. US20010031490A1th
 ; STREET: 405 Lexington Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10174
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/732,350
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/032,315
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rozek, Carol
 ; REGISTRATION NUMBER: 36,993
 ; REFERENCE/DOCKET NUMBER: 5200,200-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 599 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-732-350-6

Query Match 17.2%; Score 542; DB 10; Length 599;

Best Local Similarity 28.6%; Pred. No. 2.5e-38;
 Matches 168; Conservative 83; Mismatches 218; Indels 118; Gaps 22;

QY 49 PDGVKKEVMVNNISIIPTIFADMGDTIOYVIVNLE---TNGSTIHWGLHOKGTNL 104
 DB 35 PDGVTRNAV-LVNGRFPGLITANKGDLKITVRNKLSDPTMRSTTIHMGILQHRFAE 93

QY 105 HDGANGITECPPIPKGGRKRVYRFAKQOYSTSWHSFSAOYNGVYVGAIQINGPASTLPY- 163
 DB 94 EDGPFAVTCPIPPQESTIYTPRLGEQGTWYHSLSQYVDGLGPRIVITDPPH-PR 152
 QY 164 -----DTDGLVEPISDYYSADDELVELTKNGCAPFSVDNVLNKGAKHETGEGEYANT 218
 DB 153 NYDVDDERTVTLADWYTPSEAL-ATHVDLKITPDGTINGKGY-DPASANTNNT 210
 QY 219 L-----TPRRHRLILNTSVENHFQVSLVNHNTMCIIAADNVPVNAVYDSLEFLGV 270
 DB 211 LENLYTLKVKRCKRYRLIRINASAFSPFGVGHCKCTIIEADGYLTKPIEDADFDIAG 270
 QY 271 ORDYVIEANTPGNWNWTFEGGGLGCGSRNPYPAIF-----HAGAP----- 316
 DB 271 ORISCTLKADQDPDSWINAPITNVL-----NTNVQALLIEDDKRPTLPMKPLTWKIS 326
 QY 317 -----GGPTDEK-----APVDHNCIDLPLKPVVADVPLSG 350
 DB 327 NEIIQYQWKGHSGHKGHHKVRALIGVSGLSRVASRSADL-SKRAVLELAALVAG 385
 QY 351 FA-----KRAADTLDVTLDTTGTPLFWKVNGSA-----INIDGRAVVDVLT- QNTS 398
 DB 386 EALDKRQNEQNSTYVLETKLPIVQPCAPGSGSRADYVVLDDGLNPFANGIWTINVS 445
 QY 399 FPP-----GYNIVEVNG--ADQMSYMLIEND-----PGAPFTLPHMHLGH 439
 DB 446 YSPDPVPTLKITLTKDKVYASDFTADEHTITLPKNQVYELAIKQALGALVHPLHLGHA 505
 QY 440 EYVLGRSPDESASNERHVEDPARDAGLLSGANPRVDYSLMPLAFGVLSFRADNPGAM 499
 DB 506 FDVV-QEGDNAP-----NYNPPRRDVGVTGADG-VAIGRTDMPGW 546
 QY 500 LEFHCHIAHVSGGLGVYLERADDL-RGAVSPADADDLRLCADMR 545
 DB 547 FLHCHIDMHLLEGFAMVFAEAPEDIRKGSQSVKPPDQGMKICEYK 593

RESULT 11

US-09-944-160-12
 ; Sequence 12, Application US/09944160
 ; Patent No. US20020174452A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lewis, No. US20020174452A1man
 ; APPLICANT: Davin, Laurence
 ; APPLICANT: Huang, Ning
 ; TITLE OF INVENTION: Monocot Seeds with Increased Lignan
 ; FILE REFERENCE: WSUR117983
 ; CURRENT APPLICATION NUMBER: US/09/944,160
 ; CURRENT FILING DATE: 2001-08-30
 ; PRIOR APPLICATION NUMBER: US 60/230,632
 ; PRIOR FILING DATE: 2000-09-07
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 564
 ; TYPE: PPT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Laccase amino acid sequence from plasmid PAP1245
 ; US-09-944-160-12

Query Match 14.1%; Score 446; DB 9; Length 564;

Best Local Similarity 26.2%; Pred. No. 3.4e-30;
 Matches 142; Conservative 72; Mismatches 206; Indels 122; Gaps 21;

QY 55 EKVMLVNNISIIPTIFADMGDTIOYVIVNLENTNGSTIHWGLHOKGTNLHDGANGITRC 114
 DB 46 KSIFVYNGQFPGPTIYATBGGTIIYDVINQPSSEVNT-IHMGVKKPRPWSGPRYITQC 104
 QY 115 PIPRGGKRVYRFAKQOYSTSWHSFSAOYNGVYV-GAIOI--NGPALSPLYDT-DLGVF 170
 DB 105 PIPGANSFQKILISDELGITLWMAH--SDMSRAIVHGAIVIRPNNSNYPFRTPDAEAT 162

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Db 172 HHAAHITAEANRYRQAGIYMLTDPAEDALNPSGGEEDIMILTSKOTYANGNLVTYN 231
Qy 188 KNSGAPESDNVLENGTAKHETGEGETYANVTLPGRHRLRLINTSVENHFOVSLVNHNM 247
Db 233 GELNFWGDIYHVNCO-----PMPEKRV-----EPKKYFRFLDAVSRSGLYEADTD- 280
Qy 248 CIIAAD-WPVNAKTVDS-----LFLVGGRIVVYEANTPGNYFNENTYEGCG 295
Db 281 ---AIDTRLPEFVIVASDGLLEHPADTSLIYSMAERYVVDPSDYAK----- 327
Qy 296 ILGGSRRNPYPAPFHYAGAPGPTDEGKAPVDHNCCLPLKPVYADVPLSGFAPKA 355
Db 328 -----TIELNKGSGISGIGID-----TDYDNTD-KVMRFVADDTQPTISVVP 371
Qy 366 DNTLDVTL--DTGTPLF-----VWKVNSAINIDMGRAVVDVLTQNTSFPFGYNI 405
Db 372 ANLRVVPSPPTNTPTNPRGRTGPTWTINGVAF-----ADVQRLLAN----- 416
Qy 406 VEVNAGADMVYLIENDPCAPFTLPHPHMLGHDFYVLCRSDESPASNERHVPDPARDA 465
Db 417 VEVGTVERME--LINAGNG---WTHPHILHVDKVISR---TSGNNAFTVM--PYES 464
Qy 466 GILSGANPVRDYSMLPAGWVYL--SFRADNPGAMLFCHIAMHYSGGLGVYLERADDL 524
Db 465 GL-----KDVWLGRRRTYVVEAHYAPFPGVYMFCHNLHEDHDMMAAFNATVLPD 516
Qy 555 NCASVDADADDLRLCADWRKRYMPTNPKSDSGLKHRYVEGEGELYKA 573
Db 517 YGYNATVFVDPMEL-----WQARPYE-----LGEFOAQSGQSFVQA 553
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RESULT 14

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US-10-080-233-4
; Sequence 4, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huang
; TITLE OF INVENTION: No. US20020151450A1 Phenol Oxidizing Enzymes
; FILE REFERENCE: GCS67
; CURRENT APPLICATION NUMBER: US/10/080,233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Bilirubin oxidase
US-10-080-233-4
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Query Match 6.3%; Score 198; DB 12; Length 568;
Best Local Similarity 22.9%; Pred. No. 4.3e-09;
Matches 133; Conservative 64; Mismatches 246; Indels 138; Gaps 31;

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Qy 23 YEVDSPDTCGVNRYT---LTLLEVDMNTGPDGVVKEKVMLVNNSIIIGPTIFADMCDTIQ 78
Db 77 YEVE-----IKPTHQVYRDLGSAD-LVGYDMSR-----GPTFOVPRKVEYV 118
Qy 79 VTVINNLETNGTSIMHGLHQGTNLHDG-ANGITECPPIPPKGRKYRFRKAQOYGTSMY 137
Db 119 VAFINNAER-PRSVHLHGSFSRAA--FDGWAEDITE---PGSFKDYYPNNQASARTLMY 171
Qy 138 HS--HFSAGQY-NGVVGAIQINGRA--SLPYDTDLGVPI-----SDIYSSADELVELT 187
Db 172 HDHAMHITAEANRYRQAGIYMLTDPAEDALNPSGGEEDIPMLITSKOTYANGNLVTYN 231
Qy 188 KNSGAPESDNVLENGTAKHETGEGETYANVTLPGRHRLRLINTSVENHFOVSLVNHNM 247
Db 233 GELNFWGDIYHVNCO-----PMPEKRV-----EPKKYFRFLDAVSRSGLYEADTD- 280
Qy 248 CIIAAD-WPVNAKTVDS-----LFLVGGRIVVYEANTPGNYFNENTYEGCG 295
Db 281 ---AIDTRLPEFVIVASDGLLEHPADTSLIYSMAERYVVDPSDYAK----- 327
```

```
Qy 296 ILGGSRRNPYPAA--IFHYAGAPGPTDEGKAPVDHNCCLDPLKPVYADVPLSGFAP 353
Db 338 IGGIGTDYDITDVKVMRFVADDTQPTISVVA--NLNEDVFPSPPTNR----- 386
Qy 354 RADNTLDVTLDTGTPLFWKVGNSAINIDMGRAVVDVLTQNTSFPFGYNIYEVGADQ 413
Db 387 -----QPFEGRTG---TWTLINGVAF-----ADVQRLLAN-----VPVGTVER 422
Qy 414 WSYWLIENDPGAPFTLPHPHMLGHDFYVLCRSDESPASNERHVPD-PARDAGLLSGAN 472
Db 423 WE--LINAGNG---WTHPHILHVDKVISR---TSGNNAFTVMPEESKOVYWG--- 469
Qy 473 PYARDYSMLPAGWVYLSRADNPGAMLFCHIAMHYSGGLGVYLERADDLGANSVDAD 532
Db 470 --RRRTV-----VEAHYAPFPGVYMFCHNLHEDHDMMAAFNATVLPDYGNATVE 520
Qy 533 ADOLDRLCADWRKRYMPTNPKSDSGLKHRYVEGEGELYKA 573
Db 521 VDPMEEL-----WQARPYE-----LGEFOAQSGQSFVQA 549
```

RESULT 15

```
US-09-338-723A-2
; Sequence 2, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GCS61-2
; CURRENT APPLICATION NUMBER: US/09/338,723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-09-338-723A-2
```

Query Match 6.2%; Score 197; DB 10; Length 594;
Best Local Similarity 24.8%; Pred. No. 5.5e-09;
Matches 138; Conservative 62; Mismatches 216; Indels 140; Gaps 35;

```
Qy 33 VREYTLTLEVDMNTGPDGVVKEKVMLVNNSIIIGPTIFADMCDTIQYTVINNLETNGTSI 92
Db 107 LRPATL-----VGIDMSR-----GPTFNVRGRTYVRFINN-ATYENSV 146
Qy 93 HHGHLHQGTNLHDG-ANGITECPPIPPKGRKYRFR-KAQOYGTSMYHSH-FSAQIGN-- 147
Db 147 HLHGSFSRAP--FDGWAEDVT---FP--GEYKDYFPNNQASARLWYHDAFMKTAENAY 199
Qy 148 -GVVGAIOINGRA--SLPYDTDLGVPI-----SDIYSSADELVELTKSGAPESDNVL 199
Db 200 FQAGAYIINDAEADALGLPSGGEEDIPILITRAKTI--NADGTINSTEG-----EDDL 252
Qy 200 FNGTAKHETGEGETYANVTLPGRHRLRLINTSVENHFOVSLVNHNM-----MCTIAA 252
Db 253 W-GDVIHVGQPPPLNV---QPKRYFRFLNAAVSAMLLIYLRYSPPVRIPLFOVIAS 308
Qy 253 DMYFVVA-WTVDSLFLVGGRIVVYEANTPGNY--WFVNTYGGGLCGGSRNPYPAA- 308
Db 309 DAGLLDAPVOTSNLYLAVERYEIIIDFTNFACQTLDLRVVAFETNDV---GDEDEVARTL 365
Qy 309 -IFHYAGAPGPTDEGKAPVDHNCCLDPLKPVYADVPLSGFAPKADNTLDVTLDTTG 367
Db 366 EVMRFVYSSG---TVEDNSQV-----PSTLDVDP---PPPKRPPADHNFPE- 407
Qy 368 TPLEVWKVNSAINIDMGRAVVDVLTQNTSFPFGYNIYEVNAGADMVYLIENDPGAP 427
Db 408 -----RNSGHYILINDVGFADV---ERVLANPELGTVEY-----WELENSSGG-- 447
```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 10:43:44 ; Search time 22 Seconds

(without alignments)
2503.865 Million cell updates/sec

Title: US-09-869-877-10

Perfect score: 3158

Sequence: 1 QOOSCTPSNRACWTDGTDIN.....KSDSGIKHRWVEGEMLVKA 573

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | DB ID | Description |
|------------|--------|--------------|-------|-------------|
| 1 | 2231.5 | 70.7 | 621 2 | S72493 |
| 2 | 2032 | 64.3 | 619 1 | KSNCLD |
| 3 | 2021 | 64.0 | 619 1 | KSNCLT |
| 4 | 616 | 19.5 | 520 2 | B35883 |
| 5 | 615 | 19.5 | 520 2 | A35883 |
| 6 | 612.5 | 19.4 | 529 2 | S68120 |
| 7 | 603 | 19.1 | 520 2 | JCS356 |
| 8 | 602 | 19.1 | 520 2 | S59533 |
| 9 | 583.5 | 18.5 | 527 2 | JCS357 |
| 10 | 573 | 18.0 | 512 2 | JCS355 |
| 11 | 568 | 18.0 | 624 2 | A36962 |
| 12 | 565 | 17.9 | 572 2 | S68119 |
| 13 | 558 | 17.7 | 576 2 | S68117 |
| 14 | 556 | 17.6 | 548 2 | S18746 |
| 15 | 547.5 | 17.3 | 582 2 | T05020 |
| 16 | 542 | 17.2 | 599 2 | S68118 |
| 17 | 541.5 | 17.1 | 529 2 | S49120 |
| 18 | 531.5 | 16.8 | 533 2 | S62371 |
| 19 | 526.5 | 16.7 | 622 2 | S62380 |
| 20 | 499.5 | 15.8 | 578 2 | S66353 |
| 21 | 495.5 | 15.7 | 622 2 | S56214 |
| 22 | 490 | 15.5 | 567 2 | T44928 |
| 23 | 488 | 15.5 | 557 2 | JCS328 |
| 24 | 483.5 | 15.3 | 636 2 | A55428 |
| 25 | 475 | 15.0 | 587 1 | KSKVAD |
| 26 | 470.5 | 14.9 | 579 2 | S11027 |
| 27 | 463.5 | 14.7 | 552 2 | A51027 |
| 28 | 456.5 | 14.5 | 553 2 | T45959 |
| 29 | 453 | 14.3 | 573 2 | T02743 |

ALIGNMENTS

| | | | | | | |
|----|-------|------|-----|---|--------|---------------------|
| 30 | 450 | 14.2 | 586 | 2 | T45945 | laccase-like prote |
| 31 | 448.5 | 14.2 | 569 | 2 | T48484 | laccase-like prote |
| 32 | 448.5 | 14.2 | 570 | 2 | T00579 | probable laccase |
| 33 | 442.5 | 14.0 | 580 | 2 | F84828 | probable laccase |
| 34 | 442.5 | 14.0 | 584 | 2 | T45944 | probable laccase |
| 35 | 442 | 14.0 | 551 | 2 | T02752 | probable laccase |
| 36 | 438 | 13.9 | 554 | 2 | T01240 | laccase (EC 1.10.3) |
| 37 | 434.5 | 13.8 | 555 | 2 | T48347 | laccase-like prote |
| 38 | 415 | 13.1 | 576 | 2 | E86316 | protein T10022.11 |
| 39 | 411.5 | 13.0 | 569 | 2 | E84904 | probable laccase |
| 40 | 362 | 11.5 | 609 | 1 | KSA5L1 | laccase (EC 1.10.3) |
| 41 | 361 | 11.4 | 713 | 2 | T21201 | hypothetical prote |
| 42 | 344 | 10.9 | 632 | 2 | F83387 | copper resistance |
| 43 | 340.5 | 10.8 | 504 | 2 | F70813 | hypothetical prote |
| 44 | 333.5 | 10.6 | 611 | 2 | C82845 | copper resistance |
| 45 | 332.5 | 10.5 | 605 | 2 | S52253 | copper resistance |

RESULT 1

S72493
laccase (EC 1.10.3.2) precursor - Podospora anserina
N:Alternate names: benzenediol:oxygen oxidoreductase; urishiol oxidase
C:Species: Podospora anserina
C:Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C:Accession: S72493
R:Fernandez-Larrea, J.; Stahl, U.
Mol. Gen. Genet. 252, 539-551, 1996
A:Title: Isolation and characterization of a laccase gene from Podospora anserina.
A:Reference number: S72493; MID:97071669; PMID:8914515
A:Accession: S72493
A:Molecule type: DNA
A:Residues: 1-621 <PER>
A:Cross-references: EMBL:Y08827; NID:q1729780; PIDN:CAA70061.1; PID:q1729781
A:Experimental source: strain ATCC 26003
C:Genetics:
A:Gene: lac2
A:Insertions: 80/3; 111/1; 134/2
C:Function:
A:Description: catalyzes one-electron oxidation of mono-, di- and polyphenols, amino
C:Superfamily: laccase
C:Keywords: copper; glycoprotein; oxidoreductase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-48/Domain: amino-terminal propeptide #status predicted <PRO>
F:49-605/Product: laccase #status predicted <MOT>
F:74-209/Domain: amino-terminal beta-barrel #status predicted <BB1>
F:210-366/Domain: middle beta-barrel #status predicted <BB2>
F:431-528/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
F:606-621/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:133,261,276,289,325,334,382,401,421,441/Binding site: carbohydrate (Asn) (covalent
F:138,479/Binding site: copper (His) (type 2) #status predicted
F:140,183,185,481,548,550/Binding site: 2Cu-O cluster (His) (copper type 3) #status
F:476,549,554/Binding site: copper (His, Cys, His) (type 1) #status predicted

Query Match

Best Local Similarity 70.7%; Score 2231.5; DB 2; Length 621;
Best Similarity 68.9%; Pred. No. 7.8e-156;
Matches 397; Conservative 65; Mismatches 109; Indels 5; Gaps 4;

| | | |
|----|-----|--|
| QY | 1 | QOOSCTPSNRACWTDGTDINTEVDSPDGVRRPYLTLTEDVNTMTGPGVKEKMLV 60 |
| DB | 46 | QSSCHTANRACVAPGPDINTDEVSPTNGVTRTYLTLEVDNMLGPGVAKQKMLV 105 |
| QY | 61 | NSITIGPTIFADMGDTIOVTVINNLLETNGSIHMHGKHOKGTNLHDGANGITECPPIPKG 120 |
| DB | 106 | NGDIFGFTITANMGDWIOVAVINNLRTNGSIIHMHGKHOKGTNNHDGANGTECPPIPKG 165 |
| QY | 121 | GRKYRFAQOQYGTSTWHSFSAQYGVGAIOINPASPAPYPTDLCVPPISDIYSSA 180 |
| DB | 166 | GSRIYRFAQOQYGSWHSFSAQYGVGAIOINPASPAPYPTDIDGVPPIIDYHAKPA 225 |
| QY | 181 | DELVELKNGSGAPSDVNLNGTAKHPEDEGEVANTLTLPGRHRRLRLNTSVENHFOV 240 |

DB 492 ICRGGAISIDNLTNI-DTTLT-----NPKDTLWIOGSSWAVLRTITADPGWALH 543
QY 503 CHIAHVS-GGLGVYLERADDLRGAVSDADA-DDLDRICAD 542
DB 544 CHIGWHLETKGLAVIVQPS-----AIGHMESPESTNINCAN 580

RESULT 12

568119
laccase (EC 1.10.3.2) 3 precursor - Rhizoctonia solani
C:Species: Rhizoctonia solani
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68119
R:Wahlthier, J.A.; Xu, F.; Brown, K.M.; Brown, S.H.; Gollighly, E.J.; Halkier, T.; Kur
Curr. Genet. 29, 395-403, 1996
A:Title: The identification and characterization of four laccases from the plant pathoge
A:Reference number: S68117; MUID:96171523; PMID:8596061
A:Accession: S68119
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-572 <MAH>
A:Cross-references: EMBL:Z54215; NID:G1150565; PIDN:CAA90942.1; PID:G1150566
A:Experimental source: strain RS22
C:Genetics:
A:Gene: lcc3
A:Introns: 45/1; 81/3; 102/3; 145/1; 146/1; 186/2; 273/3; 380/3; 404/3; 441/2; 476/3; 52
C:Superfamily: laccase
C:Keywords: copper; oxidoreductase
F:1-19/Domains: signal sequence #status predicted <SIG>
F:19-572/Product: laccase 3 #status predicted <MAH>

Query Match 17.9%; Score 565; DB 2; Length 572;
Best Local Similarity 31.2%; Pred. No. 1.4e-33;
Matches 176; Conservative 60; Mismatches 206; Indels 122; Gaps 22;

QY 49 PDGVKRVKVMVNNNSIIGPTIFADMGDTQVYVNNLEFN-----GTSIHMHGIAH 103
DB 35 PDGVKRD-ATLVNGYRGGLTIFANKGDTLKVONKL-TNPMYRTTSIHMHGIAH 92
QY 104 LHDGANGITECPPIPKGGRKRYRFRKAOYGTSMYSHSFSAOYGNGVGAIOINGPASLPY 163
DB 93 DDDGAFVYTCGIYVQASTYTYMPLGDDGTGYWYHSHLSQYVDGLRGVLYIDRKD-PH 151
QY 164 -----DTDLGVFPIISDYSSADELVELTKNSGAPFSDNVLFG-----TAKHPET 209
DB 152 RRLYDIDDEKTVLILIGDWHHSKAIL-ATGNITLQGPDSATINCKGRPDONTFANPMT 210
QY 210 GEGEANTLTLPGRHRRLRLINTSVENHFOVSLVNHFMCIADADVPAVNAKYVDSLELGV 269
DB 211 -----LYTLKVRKGRKRYRLKVINNSAIASFMSIOGHKMTVIAADVSTKPYGVDSFDILA 266
QY 270 GORYDVVLEANTPGNYFNV-----TFGGGLCGGSRNPY-----PAI 309
DB 267 GORIDAVVEANDEPRTYMINAPLVANKTAQALLIEDRRPYRPRKPYRKMSVSEAI 326
QY 310 FHYAGAPGPTDEG-----KAVDHNCLDLPNLKRVVARD-----VPLS--G 350
DB 327 IKYWHKRGGLLSGHGILKARMEGSLHLHGRDLYKQNETTYVNDKTLVLEHPG 386
QY 351 FA-----KRADNTLDVTLT-----TTGTPLFWKVG-----SAINIIDGRAVVOYV 392
DB 367 AACGSKPADLVLDLTFGVNFTTGH-----WMINGIPHKSPDMPTLKLITDLDGVTESDET 442
QY 393 LTQNTSPFGYIVVEVNGADQSWYLIENDPAPFTLPHMLHGHDFVYL--GRSPDES 450
DB 443 QPEHTLILPKKNCVFEN-----IKGNSG--LGIVHPIHLHGHTEPVVQFGNNRP-- 489
QY 451 PASNERHYVDPARDAAGLISGANPVRRDYSMCLPAFGVNVLSFRPADNGAMLFCHIAHVS 510
DB 490 -----NYVNPRRRDYVGATDEG--VRFQFTDNDGPFWFLCHIDWHLE 530
QY 511 GGLGVYLERADDLRGAVSDADAD 534

DB 531 EGFANVFAEAPPAIKGPKSPVD.554

RESULT 13

568117
laccase (EC 1.10.3.2) 1 precursor - Rhizoctonia solani
C:Species: Rhizoctonia solani
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 13-Mar-1998
C:Accession: S68117
R:Wahlthier, J.A.; Xu, F.; Brown, K.M.; Brown, S.H.; Gollighly, E.J.; Halkier, T.; Kur
Curr. Genet. 29, 395-403, 1996
A:Title: The identification and characterization of four laccases from the plant pat
A:Reference number: S68117; MUID:96171523; PMID:8596061
A:Accession: S68117
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-576 <MAH>
A:Cross-references: EMBL:Z54275
A:Experimental source: strain RS22
C:Genetics:
A:Gene: lcc1
A:Introns: 45/1; 81/3; 102/3; 145/1; 146/1; 186/2; 273/3; 381/3; 405/3; 442/2; 477/3
C:Superfamily: laccase
C:Keywords: copper; oxidoreductase
F:1-19/Domains: signal sequence #status predicted <SIG>
F:20-576/Product: laccase 1 #status predicted <MAH>

Query Match 17.7%; Score 558; DB 2; Length 576;
Best Local Similarity 30.6%; Pred. No. 4.6e-33;
Matches 182; Conservative 63; Mismatches 212; Indels 138; Gaps 28;

QY 44 DMGTSPGVKRVKVMVNNNSIIGPTIFADMGDTQVYVNNLEFN-----GTSIHMHGIAH 98
DB 30 DGEIAPDG-VKRNATLVNGYRGGLTIFANKGDTLKVONKL-TNPMYRTTSIHMHGIAH 87
QY 99 QKGTNLHOGANGITECPPIPKGGRKRYRFRKAOYGTSMYSHSFSAOYGNGVGAIOI 155
DB 88 QHRNADDDGSPSVTCPIYP--RESYTYTIPLDQGTGYWYHSHLSQYVDGLRGVLYI 144
QY 156 NSPASLPY-----DTDLGVFPIISDYSSADEL-----VELTKNSGAPPS-DN 197
DB 145 YDPKD-PHRLYDVDEKTVLILIGDWHHSKAILASGITRQRYVSATINCKGRPDNP 203
QY 198 VLENGTAKHPETGEGEYANVTLPGRHRRLRLINTSVENHFOVSLVNHFMCIADDMVY 257
DB 204 -----TPANPD-----LYTLKVRKGRKRYRLKVINNSAIASFMSIOGHKMTVIAADVST 254
QY 258 NAMTVDSLEFLVGORYDYVLEANTPGNYFNV-----TFGGGLCGGSRNPY----- 305
DB 255 KPYQVADADILAGORIDCVVEANDEPRTYMINAPLVANKTAQALLIEDRRPYRPRK 314
QY 306 -----PAIFHY-----AGAPGAPPTD--EGKAPV-DHNCITDLPNLKRVYA 343
DB 315 GYRKMSVSEAITIKYWHKRGGLLSGHGILKARMEGSLHLHGRDLYKQNETTYV 374
QY 344 RD-----VPLS--GFA--KRADNTLDVTLT-----TTGTPLFWKVG-----SA 379
DB 375 MDESKVLPLEYGAAGSKPADLVLDLTFGLNFATGH-----WMINGIPYESKPIPLKI 430
QY 380 IINIDGRAVVOYVLTQNTSPFGYIVVEVNGADQSWYLIENDPAPFTLPHMLHGH- 438
DB 431 LTDEGVESDETKEHEVYILPKKNCIEFN-----IKGNSGIPIT--HVIHLHGT 479
QY 439 -DFYVLSRSPDES PASNERHYVDPARDAAGLISGANPVRRDYSMCLPAFGVNVLSFRADNG 497
DB 480 WDVVQFGNNRP-----NYVNPRRRDYVGATDEG--VRFQFTDNDGPFWFLCHIDWHLE 518
QY 498 AMLFCHIAHVSGLGVYLERADDLRGAVSDADAD-DLDRICADWRRYFNP 551
DB 519 PWFILCHIDWHLEEGFANVFAEAPPAIKGPKSPVD.554

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 10:03:34 ; Search time 14 Seconds

(without alignments)
1697.567 Million cell updates/sec

Title: US-09-869-877-10

Perfect score: 3158
Sequence: 1 Q0SCNTPSNRACWTGIDIN.....KSDGLKHRYWEGEMLVKA 573

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|--------|--------------------|-------|-------------|
| 1 | 2231.5 | 70.7 | 621 1 | LAC2_PODAN |
| 2 | 2032 | 64.3 | 619 1 | LAC1_NEUCR |
| 3 | 2021 | 64.0 | 619 1 | LAC2_NEUCR |
| 4 | 1849 | 58.5 | 591 1 | LAC1_CRYPA |
| 5 | 824.5 | 26.1 | 486 1 | LAC1_BOTCI |
| 6 | 636 | 20.1 | 520 1 | LAC1_TRAVI |
| 7 | 615 | 19.5 | 520 1 | LAC1_CORHI |
| 8 | 603 | 19.1 | 520 1 | LAC4_TRAVI |
| 9 | 602 | 19.1 | 520 1 | LAC5_TRAVI |
| 10 | 583.5 | 18.5 | 527 1 | LAC5_TRAVI |
| 11 | 580.5 | 18.4 | 527 1 | LAC5_TRAVI |
| 12 | 571 | 18.1 | 519 1 | LAC2_TRAVI |
| 13 | 570 | 18.0 | 519 1 | LAC3_TRAVI |
| 14 | 565 | 17.9 | 572 1 | LAC3_THACU |
| 15 | 564 | 17.9 | 531 1 | LAC4_THACU |
| 16 | 558 | 17.7 | 576 1 | LAC1_THACU |
| 17 | 556 | 17.6 | 548 1 | LAC1_PHLRA |
| 18 | 546.5 | 17.3 | 520 1 | LAC2_AGABI |
| 19 | 541.5 | 17.1 | 529 1 | LAC1_PLEOS |
| 20 | 541 | 17.1 | 599 1 | LAC2_THACU |
| 21 | 531.5 | 16.8 | 520 1 | LAC1_AGABI |
| 22 | 531.5 | 16.8 | 533 1 | LAC2_PLEOS |
| 23 | 526.5 | 16.7 | 622 1 | YAB8_SCHPO |
| 24 | 510.5 | 16.2 | 473 1 | LAC3_TRAVI |
| 25 | 499.5 | 15.8 | 578 1 | ASO_TOBAC |
| 26 | 495.5 | 15.7 | 622 1 | FER3_YEAST |
| 27 | 483.5 | 15.3 | 636 1 | FER3_YEAST |
| 28 | 475 | 15.0 | 587 1 | ASO_CUCSA |
| 29 | 474.5 | 15.0 | 579 1 | ASO_CUCMA |
| 30 | 472.5 | 15.0 | 624 1 | ASO_CUCMA |
| 31 | 463.5 | 14.7 | 609 1 | ASO_CUCPM |
| 32 | 362 | 11.5 | 552 1 | LAC1_EMENT |
| 33 | 332.5 | 10.5 | 605 1 | PCOA_BCOLI |

| | | | | |
|----|-------|------|-------|-------------|
| 34 | 328.5 | 10.4 | 608 1 | YD56_YEAST |
| 35 | 319 | 10.1 | 609 1 | COPA_PSESMA |
| 36 | 254.5 | 8.1 | 554 1 | NTF3_TOBAC |
| 37 | 252 | 8.0 | 516 1 | CUEO_ECOS7 |
| 38 | 249.5 | 7.9 | 555 1 | ASO_BRANA |
| 39 | 249 | 7.9 | 516 1 | CUEO_BCOLI |
| 40 | 230 | 7.3 | 536 1 | CUEO_SALTI |
| 41 | 228 | 7.2 | 536 1 | CUEO_SALTY |
| 42 | 227 | 7.2 | 513 1 | CORA_BACSU |
| 43 | 204 | 6.5 | 572 1 | BULO_MYRVE |
| 44 | 200 | 6.3 | 533 1 | CUEO_YEAP |
| 45 | 162 | 5.1 | 642 1 | PHSA_STRAT |

ALIGNMENTS

RESULT 1
LAC2_PODAN
ID LAC2_PODAN STANDARD: PRT: 621 AA.
AC P78722;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Laccase II precursor (EC 1.10.3.2) (benzenediol:oxygen oxidoreductase)
DE (Urishiol oxidase) (diphenol oxidase) (laccase C).
GN LAC2.
OS Podospora anserina.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Lasiosphaeriales; Podospora.
OX NCBI_TaxID=5145;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 26003;
RX MEDLINE=97071669; PubMed=8914515;
RA Fernandez-Larrea J., Stahl U.;
RT *Isolation and characterization of a laccase gene from Podospora
RT anserina*;
RT Mol. Gen. Genet. 252:539-551(1996).
RL
CC -1- FUNCTION: PROBABLY INVOLVED IN LIGNIN DEGRADATION AND IN THE
CC DETOXIFICATION OF LIGNIN-DERIVED PRODUCTS IN ITS NATURAL HABITAT
CC (HERBIVOROUS DUNG), WHICH IS RICH IN LIGNIN OF GRASSES AND STRAW.
CC PROBABLY INVOLVED IN MELANIN SYNTHESIS AND IN PERTHECIA
CC DEVELOPMENT.
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzosemiquinone + 2
CC H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: LOW BASIC LEVELS THROUGHOUT THE GROWTH PHASE;
CC INCREASES AT LEAST 20-FOLD AT THE BEGINNING OF THE AUTOLYTIC PHASE
CC AND DECREASES AGAIN THEREAFTER.
CC -1- INDUCTION: UNDER OXIDATIVE STRESS ON THE MYCELIUM BY AROMATIC
CC XENOBIOTICS (GUARACOL, HYDROQUINONE, BENZOQUINONE), AND BY COPPER
CC SALT AT A CONCENTRATION OF 1mM (GROWING MYCELIUM).
CC -1- PTM: LACCASE II IS PROCESSED AT BOTH ITS N-TERMINUS AND ITS C-
CC TERMINUS.
CC -1- MISCELLANEOUS: PODOSPORA ANSERINA CONTAINS AT LEAST 3 LACCASE
CC ISOFORMS NAMED I, II, AND III. THEY DIFFER IN THEIR SUBSTRATE
CC SPECIFICITY, NUMBER OF SUBUNITS, ISOELECTRIC POINT AND HEAT
CC STABILITY.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

FT PROPER 607 619 PLASTOCYANIN-LIKE 1.
 FT DOMAIN 84 207 PLASTOCYANIN-LIKE 2.
 FT DOMAIN 216 373 PLASTOCYANIN-LIKE 3.
 FT DOMAIN 431 566 PLASTOCYANIN-LIKE 3.
 FT METAL 144 144 COPPER (TYPE 2) (PROBABLE).
 FT METAL 146 146 COPPER (TYPE 3) (PROBABLE).
 FT METAL 189 189 COPPER (TYPE 3) (PROBABLE).
 FT METAL 191 191 COPPER (TYPE 3) (PROBABLE).
 FT METAL 477 477 COPPER (TYPE 1) (PROBABLE).
 FT METAL 480 480 COPPER (TYPE 2) (PROBABLE).
 FT METAL 482 482 COPPER (TYPE 3) (PROBABLE).
 FT METAL 548 548 COPPER (TYPE 3) (PROBABLE).
 FT METAL 549 549 COPPER (TYPE 1) (PROBABLE).
 FT METAL 550 550 COPPER (TYPE 3) (PROBABLE).
 FT METAL 554 554 COPPER (TYPE 1) (PROBABLE).
 FT METAL 559 559 COPPER (TYPE 1) (PROBABLE).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 422 422 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 619 AA; 68198 MW; FDEDD6D78B65048E3 CRC64;

Query Match 64.3%; Score 2032; DB 1; Length 619;
 Best Local Similarity 64.3%; Pred. No. 3.3e-137;
 Matches 359; Conservative 80; Mismatches 113; Indels 6; Gaps 2;

QY 4 CPTSPNACWMTGDIYNDIEYDSDPTGVVPRYTLLTFVDMWGTGPDGVKVKMLVNN 63
 DB 55 CNSPFRNROCHSGFENINDYELGTNTGKTKKILFTETDMWIGPDYIKKVMVNDK 114
 QY 64 IIGPTIFADMGDTIOVTVINNETNGSTIHWGLHOKGTNLHDGANGITECPDIPKGRK 123
 DB 115 IIGPTIADMGDIETVIVINKLNGSTSIHWGMHQRNINODGVNGVTECPDIPKGRK 174
 QY 124 VYRFRAGQGTSMYSHSFAOYNGVGAIOINGPASLPIYDIDLGAFPSIDVYYSADL 183
 DB 175 VYRFRAGQGTSMYSHSFAOYNGVGAIOINGPASLPIYDIDLGAFPSIDVYYSADL 234
 QY 184 VELTKNSGAFSDNYLFGNTAKHPETGESEYANVLTTPGRHRLRLINTSVENHFQVSLV 243
 DB 235 VLLTGHAGSPNNVLFNFPAKHPTTGAGQYATVSLTKGKRRLRLINTSVENHFQVSLV 294
 QY 244 NHTTCLIAADMYPVNMMYVLSLFLVGORYDYVIEANRTPGYVWENVTFGSLCGGSRN 303
 DB 295 NHTTCLIAADMYPVNMMYVLSLFLVGORYDYVIEANRTPGYVWENVTFGSLCGGSRN 354
 QY 304 PYPALIFHAGAGPDPDEGKAPVDHNCGLD.PNLKPVVARVPLSGFKAADNTLADVTL 363
 DB 355 PYPALIFHAGAGPDPDEGKAPVDHNCGLD.PNLKPVVARVPLSGFKAADNTLADVTL 414
 QY 364 DTTGPTLFWYKNGSAINIDMGRAVVDYVLTQNTSPFPGYNIVEVNGADOMSWYLENDP 423
 DB 415 DG-----FWVRNGTAININMNMKPYLEYVLTGNTNVSQSDNIVQYGVGMKYLENDP 469
 QY 424 GAPETLPHMHLGHDFYVLSRSPDESANRHYFDPARADGLSGANPVRRDYSMLPA 483
 DB 470 DGAFSLPHRHLGHDFYVLSRSPDESANRHYFDPARADGLSGANPVRRDYSMLPA 529
 QY 484 FGMVYLSFRADNGAMVLFCHIAMHVSGLGVYVLELRADLKGAVYLRADLDRACAD 543
 DB 530 KGMVYLSFRADNGAMVLFCHIAMHVSGLGVYVLELRADLKGAVYLRADLDRACAD 589
 QY 544 RRYWPTN-PYPRKSDGLK 560
 DB 590 RAYFPDNNAPFKDSDGLR 607

DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Laccase precursor (BC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
 DE (urishiol oxidase) (Laccase allele 75).
 GN LACC.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86087214; PubMed=2961749;
 RA German U.A., Mueller G., Hunziker P.E., Larch K.;
 RT "Characterization of two allelic forms of Neurospora crassa laccase.
 RT Amino- and carboxyl-terminal processing of a precursor";
 J. Biol. Chem. 263:885-896(1988).
 CC -1- FUNCTION: LIGNIN DEGRADATION AND DEOXYFICATION OF LIGNIN-DERIVED
 CC PRODUCTS (PROBABLE).
 CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzenesemiquinone + 2
 CC H(2)O.
 CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
 CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
 CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOOPER OXIDASES.
 CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
 CC -----
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL_M18334; AAA33592.1; -
 DR PIR_B28523; KSNCLT.
 DR InterPro: IPR001117; Cu-oxidase.
 DR InterPro: IPR002355; Multicu_oxidase2.
 DR Pfam: PF00394; Cu-oxidase; 3.
 DR PROSITE: PS00079; MULTICOOPER OXIDASE1; 1.
 DR PROSITE: PS00080; MULTICOOPER OXIDASE2; 1.
 KM Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
 KM Glycoprotein; Repeat.
 FT SIGNAL 1 21
 FT PROPEP 22 49
 FT CHAIN 50 606
 FT PROPEP 607 619
 FT DOMAIN 84 207
 FT DOMAIN 216 373
 FT DOMAIN 431 566
 FT METAL 144 144
 FT METAL 146 146
 FT METAL 189 189
 FT METAL 191 191
 FT METAL 477 477
 FT METAL 480 480
 FT METAL 482 482
 FT METAL 548 548
 FT METAL 549 549
 FT METAL 550 550
 FT METAL 554 554
 FT METAL 559 559
 FT CARBOHYD 139 139
 FT CARBOHYD 282 282
 FT CARBOHYD 295 295
 FT CARBOHYD 340 340
 FT CARBOHYD 422 422
 FT CARBOHYD 444 444
 SQ SEQUENCE 619 AA; 68120 MW; 0BB6CDE18841145 CRC64;

Query Match

64.0%; Score 2021; DB 1; Length 619;


```

Db 333 GRSNNPFAAIIHYGASNSHPTKGVAPADHECLDLNLVYVPRSLTSGFVAASDNT 392
Qy 359 LDVLTDTGTPLFWKVGSAINIDMGRAVDYVLTONTSPFPQYIYEVNGADQMSYWL 418
Db 393 LDVQSTTRK---WTINGSTLDVDMGHPIYOYINKSTAMSTNDVNLVEEAGNOMAYWL 449
Qy 419 IENDGAP-FITLPHPMHLHGHDFTYVLSGSPDESASNERHVPDPARDGLSGANPRRD 477
Db 450 IENDPTAGNMLPHPIHGHGDFVILGRSPNVSPTAQTPYTP-TSSDVSLSLGNNDPIIRD 508
Qy 478 VSNLPAFGVWVLSFRADNPGAWLFHCHIAHVSGLGVYTLERRADDLRAVSDADADD 537
Db 509 VVNLPPKMLLAFQTTNPGAMLMCHIAHVSAGLGTFLKPSAFVAGLNTNDVNLQNL 568
Qy 538 RLCAADRRYTPNP-YPKSDGL 559
Db 569 SQCKSMNAYYPSKIDFKODDSGV 591

RESULT 5
LACL BOTCI STANDARD: PRT: 486 AA.
ID LACL BOTCI
AC 012570:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE laccase (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase) (Urisiol
oxidase) (Diphenol oxidase) (Fragment).
GN LACL.
OS Botrytis cinerea (Botryotinia fuckeliana).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OX Helotiales; Sclerotiniaceae; Botryotinia.
RN NCBI_TaxID=40559;
RP [1]
RC SEQUENCE FROM N.A.
RA Cantone F.A.; Staples R.C.;
RT "A laccase cDNA from Botrytis cinerea.";
RL Phytopathology 83:1383-1383(1993).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
PRODUCTS (PROBABLE).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzenesemiquinone + 2
H(2)O.
CC -1- COPACITOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A STOP CODON HAD TO
BE SKIPPED IN POSITION 346 TO PRODUCE THIS ORF.
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CC -----
DR EMBL: U20192; AAA41823.1; ALT_SEQ.
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicu_oxidase2.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER OXIDASE1; 1.
DR PROSITE: PS00080; MULTICOPPER OXIDASE2; 1.
KM Oxidoreductase; Copper; Metal-binding; Lignin degradation;
FT Glycoprotein; Repeat.
FT NON_TER 1
FT DOMAIN <1 84 PLASTOCYANIN-LIKE 1.
FT DOMAIN 132 238 PLASTOCYANIN-LIKE 2.
FT DOMAIN 287 446 PLASTOCYANIN-LIKE 3.

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FT METAL 5 5 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 7 7 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 66 66 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 68 68 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 370 370 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 373 373 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 375 375 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 429 429 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 430 430 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 431 431 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 435 435 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 435 435 COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 486 AA; 52567 MW; 19782C3E4108FE4D CRC64;

Query Match 26.1%; Score 824.5; DB 1; Length 486;
Best Local Similarity 34.4%; Pred. No. 2,1e-51;
Matches 176; Conservative 75; Mismatches 195; Indels 65; Gaps 12;

Qy 89 GTSIHWHGCHOKSTNLHDC-----ANQITPCPIPPKGGRYVFRKAAQ 131
Db 1 GTTMHWHGIROLNMAQYDVPKRGKSYSIPYHKLTLSTGITOCPNAP-GGTLTYKHADN 59
Qy 132 YGTSWYHSHFSQYGVGVGAIOINGPASPYPDTDGVPIPSDYSSADELVELFKNSG 191
Db 60 YGSSWYHSHFIIYDGGGLGPELVINGPATANDVDGLMFLNDMNHVPQSLMDRAKTA 119
Qy 192 APFSDVNLFGNGAKHPEBEGEYANTYLPGRHRLRLINTSEVNHFOYSLVNHWCITA 251
Db 120 PFTLTGLMNGTWY--NGAGKKFQTFPGLKYRIRVNTAVDGHFQSIDGHSFOVYA 177
Qy 252 ADMVPPVNAATVDSIFLGVQGRDVYVEANRTGNTVFNTFFGGGLCGSSRRPY-ALF 310
Db 178 MDEVPVPPVNAATVDSIFLGVQGRDVYVEANRTGNTVFNTFFGGGLCGSSRRPY-ALF 310
Qy 311 HVGAGG-GPPDEGKAPVDHNCIDLPNLKPVARVPVPSGFAKRDNTLDVTLDTGTGP 369
Db 236 RTYGSSSTADPTTTSVTVASTSLDEP-----LASLVPVPVPIPIASSIMKTLTITGGGQ 290
Qy 370 LEVWYKVSAINIDMGRAVDYVLTONTSPFPQYIYEV-----NGAD 412
Db 291 ---WLENGSSILMTMTDPTLTVLNSGNIMPEYVNIPIESTAKKMAVLAISGPNXA 347
Qy 413 QMSY---WLENDGAPFLTP-HPMHLHGHDFTYVLSGSPDESASNERHVPDPARDAGLL 468
Db 348 FYHYPPIILISNHTDMLFSSPNHPIHLHGHDFTYVLSGSPDESASNERHVPDPARDAGLL 395
Qy 469 SGANPYRDPVSMPLAFGVWVLSFRADNPGAWLFHCHIAHVSGLGVYTLERRADDLRAV 528
Db 396 NLVNPFRDRLVLTSTGHLVIAFQIDNPGSWLMHCHIAHVSAGLGTFLKPSAFVAGLNTNDV 455
Qy 529 SDDADDDLRLCADWRRYTPNPYPKSDGL 559
Db 456 GTADVSTFONTCAMKGMPTPEPFPQDDSGI 486

RESULT 6
LACL TRAVI STANDARD: PRT: 520 AA.
ID LACL TRAVI
AC 099044:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE laccase I precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
(Urisiol oxidase) (Diphenol oxidase).
GN LACL.
OS Trametes villosa (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

```

Db 256 SIQLEAQRYSFVLNADDDVGNMYTIRANPNNGNNGVFAAGGIN-----SALIRFDGADPVEPT 311
 QY 322 DEGAAPDHNCGLDIPNKFPVYARADYPLSGFAKKRADNILDITLDITGTPPLFWKNGNSAI- 380
 Db 312 TTQTPPT--KPLNEVDLHPLATMAVPGSPVAGVDITALNMAFNNGINTF--INGASEV 366
 QY 381 --NIDMGAVVDVYVLTQNTSEPPG--YVIVEVNGADQMSYMLIENDPCAPETLPHPMILH 436
 Db 367 PPTVPLVLLQIISGAGNMADLLPSGSYSLSPS-NMDIELSFATAAPCA-----PHPLFLH 421
 QY 437 GHDFVYLGSRPDESPASNERHVFDPARDAG--LLSGANPVRRDY--SKLPAPG-VWVLSF 491
 Db 422 GHAAVYV-----RSAGSTVYNNTDPIPRDYVSTGTGPAAGNVITRF 462
 QY 492 RADNPAGWLFICHTIAMHYSGLGVYVYLERADLDNGAVSDADADDLDRICADWRRRYPTNP 551
 Db 463 RTDNPGEPLFLCHCHIDFHLHAGFAVFAEDIDVASA-----NP 500
 QY 552 YPKSDSGL 559
 Db 501 VPOAMSDL 508
 RESULT 8
 LAC4_TRAVI STANDARD: PRT: 520 AA.
 ID LAC4_TRAVI
 AC OQ9055;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Laccase 4 precursor (EC 1.10.3.2) (benzenediol: oxygen oxidoreductase)
 GN (Diflavin oxidase) (Diphenol oxidase).
 NC LCC4.
 OS Trametes villosa (White-rot fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Trametes.
 RX NCBI_TaxID=47662;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97128774; PubMed=8973314;
 RA Yaver D.S., Golightly E.J.;
 RT "Cloning and characterization of three laccase genes from the
 RT white-rot basidiomycete Trametes villosa: genomic organization of the
 RT laccase gene family.";
 RL Gene 181;95-102(1996).
 CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
 CC PRODUCTS (PROBABLE).
 CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
 CC H(2)O.
 CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE, THREE DISTINCT CU
 CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
 CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
 CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L78077; ABA47734.1; -
 DR HSSP: P37064; IASO.
 DR InterPro: IPR001117; Cu-oxidase.
 DR InterPro: IPR002355; Multicu_oxidase2.
 DR Pfam: PF00394; Cu-oxidase; 3.
 DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
 DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
 KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;

| FT | CABOBYND | 497 | 497 | N-LINKED (GILCNC. . .) (POTENTIAL). |
|------------|--|---|-----------|-------------------------------------|
| SQ | SEQUENCE | 520 AA; | 55643 MW; | FC1032400E9DDFAA CXC64; |
| | Query Match | | 19.1%; | Score 602; DB 1; Length 520; |
| | Best Local Similarity | | 32.0%; | Pred. No. 1.5e-35; |
| | Matches 179; | Conservative | 77; | Mismatches 211; Indels 92; Gaps 24; |
| QY | 30 | TCGVNPPY-LTLEEDVNTGPGGVKKEKYMVNNSIGPTLEADMGDTLTQVTVNNL--E | 86 | |
| DB | 21 | SAAGPPTDLTISNAD--VSPDGFTRAAV-LANGVFPGLITNGKGNDFQIIVIDLNSNE | 77 | |
| QY | 87 | T--NCTSIHHMGLHCKGTNLNHDGANGITECPIPPKGRKRYRFKA-QOYGISWYSHFSA | 143 | |
| DB | 78 | TMLKSTSIHHMGEFQCKTNMADGAFAVNOCP-ATGNSPLFYDTATDAGTFWYHSHST | 136 | |
| QY | 144 | OYGNGVCAIQINGNASLPY-----DDLDGFPISDYIYSSADELVETKNSGAF--- | 194 | |
| DB | 137 | QYCDLRKPMVYVDDPSD--PHADLYVDDETITLTLSDMWHFA-----SLGAAPIG | 187 | |
| QY | 195 | SDNVLENGTAKHPETEGEYEANVTLTGPRNRLRLINTSVENHFOVSLVHTMCIITADM | 254 | |
| DB | 188 | SDSTLNLGRRAGGDSYDLAVITVEQGRKRYMRRLSLSCDPNYEFSIDGHMTIIEADA | 247 | |
| QY | 255 | VPVNAAMYDSLFLVGQGRDYVEANKRPQNTW-----NVTFGGGLCGGRNRYPA | 307 | |
| DB | 248 | VNHEPLTADYSIDYVQGRYSEFLTQADODIDNFIYALPSAGTTSFGDGI-----NS | 298 | |
| QY | 308 | ALFHHVAGGPGPPTEDEKAPVDHNCLDLPLNKPVYAROVPLSGFRKRNADNTLDTLTG | 367 | |
| DB | 299 | ALIKRSGASEVDPPTTETTSV--LELDENALVPLDSPAAPGDPNIGGVADYALNLDPNFDG | 356 | |
| QY | 368 | TPLEWYKNGSAINIDWGRAVVDYVLTGNTS---FPPG-YNIVVENGADQMSYML-IEB | 421 | |
| DB | 357 | TNFFINDVSFVSPVY-----PYLLQILSGTTSADLLPQSLFALPSNSTIEISFPITATN | 412 | |
| QY | 422 | DGGAFTLPHPHNLHGDFYVILGRSPDSSPANSERHVEDPADAGL--LSGANPVRDYS | 479 | |
| DB | 413 | APGA-----PHPHNLGHFTSTV-----RTASGTDTFNFPVRDDV | 449 | |
| QY | 480 | MLPAFG-WVYLSFRANDNGAMFLHCHIAMHVSGLGVYLERADDLRGAVSDADDDLLR | 538 | |
| DB | 450 | NTGTAGDVNTIRFTDNDQPMFLHCHIDPHELAGPAIVSEDTADVSNITTPSTA----- | 504 | |
| QY | 539 | LCADMRRKTYPT-NRYPKSD | 556 | |
| DB | 505 | ---MEDLCPTYNALDSSD | 519 | |
| RESULT 10 | | | | |
| LACS_TRAVI | | | | |
| ID | LACS_TRAVI | STANDARD: | PRT: | 527 AA. |
| AC | Q09056; | | | |
| DT | 01-NOV-1997 (Rel. 35, Created) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) | | | |
| DE | Laccase 5 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase) | | | |
| DE | (Urishiol oxidase). | | | |
| GN | LCCS. | | | |
| OS | Trametes villosa (White-rot fungus). | | | |
| OC | Eukaryota, Fungi, Basidiomycota; Hymenomycetes; Homobasidiomycetes; | | | |
| OC | Ascomycota; Basidiomycota; Hymenomycetes; | | | |
| OX | NCBI_TaxID=47662; | | | |
| OX | NCBI_TaxID=47662; | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RP | MEDLINE=97128774; PubMed=8973314; | | | |
| RA | Yaver D.S., Gollightly E.J.; | | | |
| RT | "Cloning and characterization of three laccase genes from the | | | |
| RT | white-rot basidiomycete Trametes villosa: genomic organization of the | | | |
| RT | laccase gene family." | | | |
| RL | Gene 181:95-102(1996). | | | |
| RP | REVISIONS. | | | |
| RA | Yaver D.S., Gollightly E.J.; | | | |

[illegible]

Db 355 SFSNGSNFFINNETPVPVYLQILSGADAAASLNGSV-----YTLPSNS 403

QY 398 SFPQGVNIVEVNGADQMSWYLNDPGAPFTLPHPMHLGHDFVYLGKSPDESPASNERH 457

Db 404 TIEISFPIITDGA-----LNAPGA-----PHEFLHGHTEFSV----- 437

QY 458 VFEDARQAG--LLSGANPVARD--VSMLEPFGWYLSFADNPGAMFLFCHTAMHVSGLG 514

Db 438 -----RSAGSSTFYANVRDVTGNSGDNVTRFTTDNPGFWEFLHCHIDFLADGFA 492

QY 515 VVLERADDLRGAVSDADADLDRICADRRKRYMPTNPKSDS 557

Db 493 IVFAE-----DTADTASANPVPTAMSDLCPT--YDALDS 524

RESULT 12

LAC2_TRAVI STANDARD; PRT; 519 AA.

AC 099046;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Laccase 2 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)

GN (Uristiol oxidase) (Diphenol oxidase).

OS LCC2.

OC Trametes villosa (white-rot fungus).

OC Eukaryote; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

OX Aphyllophorales; Trametes.

OX NCBI_TaxID=47662;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Mycelium.

RX MEDLINE=97076915; PubMed=8975613;

RA Xaver D.S., Xu F., Gollighly E.J., Brown K.M., Brown S.H.,

RA Ray M.W., Schneider P., Halkier T., Mondorf K., Dalboge H.;

RT "Purification, characterization, molecular cloning, and expression of

RT two laccase genes from the white rot basidiomycete Trametes

RT villosa.";

RL Appl. Environ. Microbiol. 62:834-841(1996).

CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED

CC PRODUCTS (PROBABLE).

CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzoquinone + 2

CC H(2)O.

CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU

CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE

CC 3 OR COUPLED BINOCLEAR (BY SIMILARITY).

CC -1- SUBUNIT: HOMODIMER.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.

CC -----

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CC or send an email to license@sib-sib.ch).

CC -----

CC EMBL: LA9377; AAC41687.1; .

DR HSSP: P37064; LAOZ.

DR InterPro: IPR001117; Cu-oxidase.

DR InterPro: IPR002355; Multicu_oxidase2.

DR Pfam: PF00394; Cu-oxidase 3.

DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.

DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.

DR Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;

KM Lignin degradation; Multigene family.

FT SIGNAL 20 POTENTIAL.

FT CHAIN 1 519 LACCASE 2.

FT DOMAIN 22 147 PLASTOCYANIN-LIKE 1.

FT DOMAIN 159 301 PLASTOCYANIN-LIKE 2.

FT DOMAIN 368 490 PLASTOCYANIN-LIKE 3.

FT METAL 84 84 COPPER (TYPE 2) (BY SIMILARITY).

FT METAL 86 86 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 129 129 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 131 131 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 415 415 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 418 418 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 420 420 COPPER (TYPE 2) (BY SIMILARITY).

FT METAL 422 422 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 473 473 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 474 474 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 478 478 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 478 478 COPPER (TYPE 1) (BY SIMILARITY).

FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 519 AA; 55777 MM; DB4EA526F684740 CRC64;

Query Match 18.1%; Score 571; DB 1; Length 519;

Best Local Similarity 29.7%; Pred. No. 2,5e-33;

Matches 162; Conservative 75; Mismatches 200; Indels 108; Gaps 22;

QY 49 PDGVKREKVMVNNSSIPTIFADWDGTIOYVINNLFTN-----CTSIHMHGLHOKGTNL 104

Db 37 PDGFLRDAL-VVNGVVPPLITGKGRDFOLNVDTLNNHSMKSTSIHMGCFRAGAGNW 95

QY 105 HDGANGITECPPIPKGGRKRYRFA-NQGYTSWHSRPSAOGNGVCAIOI---NGPAS 160

Db 96 AEGPAFVNQCP1-ASGHSEFLYDFHVPDQAGTFYHSHSLSTGYCDLRSRPFVYDPRDHA 154

QY 161 LPYPRD--LGFPISDYYSDELVELTKNSGAF-----SDNVLENGAKHPEGEGEYTA 215

Db 155 SRIDVNDNSTYITLIDWYHIA-----RLGKFPPLGADNTLNGRSASTYALA 206

QY 216 NVTLTPGRHRLRLINTSVENHFOVSLVNHHTCITAADMVPVNAATVSLFVGQRYDV 275

Db 207 VINQHGKRYRFLYSICDNYTFSDIGNHLTVIEVDGINSQPLVDISQIFAQRRSF 266

QY 276 VIEAKRTGNTWF--NTFFGGGLCGSRNPPAIFHAGAPGPPDEGKAPVDHNCI 333

Db 267 VLNMQTGNWVRANPNEFTGVFAGGIN---SALILEYOGAPVAEPPTTQTPSV----- 317

QY 334 DLP-----NLKPVVADVPLSGFAKRAADNTLDVTDYTGPLEVWKNVNSA-----I 380

Db 318 -IPLETLHLHARIPVCGSTPPGCVDAKALNAFENGTNFF---INNAITPTTPVYVL 373

QY 381 NIDWGRAVVDVLTQNTSP-PGYNIVEVNGADQMSWYLNDPGAPFTLPHPMHLGHGD 439

Db 374 QILSGAQAOQLDLPAGSVYPLPAHSTIEI-----TLPATLAPGA-----PHEFLHGH 423

QY 440 FVYLGSRDESPASNERVFPDARAG--LLSGANPVARDV--SMLEPFG-VWYLSFAD 494

Db 424 FAVV-----RSAGSTYNYNDPIRDVASTGPAAAGNVITRFQTD 464

QY 495 NPGAMLFCHTAMHVSGLGAGVYLERADDLRGAVSDADADLDRICADRRKRYMPTNPK 554

Db 465 NPGWFLHCHIDFLHDAFAIYFADVADYKAA-----NPPPK 502

QY 555 SDSGL 559

Db 503 AMSDL 507

RESULT 13

LAC2_TRAVE STANDARD; PRT; 519 AA.

AC 012718; 012716;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

| | | |
|-------------|--|---|
| QY | 270 | GORDVVEIARTGTGNYENF-----TGGGLLCCGSNRP-----PAI 309 |
| Dy | 267 | GORDVAVEAENDEPTVINAPLTWANKTAOLLITYEDDRPRPHPKPYRKMSVSEAI 326 |
| QY | 310 | FHYGAPCGPPTDES----KAVDHNCITDLNLKPVRVD-----VPLS--G 350 |
| Dy | 327 | IKYMKHKGRCLLSCHGGLKARMBEGSLHLGRDRIYKRONETTTVVMDERTKVLEHPG 386 |
| QY | 351 | FA-----KRAIDLDTLD---TTGPFLPYWKNG-----SAINIDGRAVDYV 392 |
| Dy | 387 | AAGSKSPADVLIDTLFGVNFTTG----WMINGIPHSBDPMPTLLKITLDDGVGESDFT 442 |
| QY | 393 | LTONTSPPPCGYNIYEVNACDOMSTYLINDDGAPTLPRLPHMLHGCHDYVL--GSPDES 450 |
| Dy | 443 | QPERTILLPKRKCVEFN-----IKNGSG--LGIVPIHLHGHTDVVOFGNNP-- 489 |
| QY | 451 | PASNERHVDPBARAGLLSGANPVRYDSMULPAFGVYVLSFRADPGAMLFPHCHIAHVS 510 |
| Dy | 490 | -----NYPNPBRDVGATDES-VRFQRTDNPGFWFLCHIDWHILE 530 |
| QY | 511 | GGLGVYLERADDLRGAVSDAD 534 |
| Dy | 531 | EGFMAVFEADEALIKGPKSVPD 554 |
| <hr/> | | |
| RESULT 15 | | |
| LACC4_THACU | | |
| ID | LACC4_THACU | STANDARD; PRT: 531 AA. |
| AC | 002081; | |
| DT | 01-NOV-1997 (Rel. 35, Created) | |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) | |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) | |
| DE | Laccase 4 precursor (Ec 1.10.3.2) (benzenediol:oxygen oxidoreductase) (Trishiol oxidase) (Diphenol oxidase). | |
| GN | LCC4. | |
| OS | Thaneophorus cucumeris (Black scurf of potato) (Rhizoctonia solani). | |
| OC | Eukaryote; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; | |
| OC | Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae; | |
| OC | Mitosporic Ceratobasidiaceae; Rhizoctonia. | |
| OX | NCBI_TaxID=107832; | |
| RN | [1] | |
| RP | SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. | |
| RC | SRRAIN-RS22; | |
| RX | MEDLINE=36171523; PubMed=8598061. | |
| RA | Waltheimer J.A., Xu F., Brown K.M., Brown S.H., Golightly E.J., | |
| RA | Halkier T., Kauppinen S., Pederson A., Schneider P.; | |
| RT | "The identification and characterization of four laccases from the | |
| RT | plant pathogenic fungus Rhizoctonia solani."; | |
| RU | Curr. Genet. 29:395-403(1996)." | |
| -1- | FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED | |
| CC | PRODUCTS (PROBABLE). THIS ISOZYME SHOWS OPTIMAL ACTIVITY AT PH 7. | |
| CC | -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzosemiquinone + 2 | |
| CC | H(2)O. | |
| CC | -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU | |
| CC | CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE | |
| CC | 3 OR COUPLED BINUCLEAR (BY SIMILARITY). | |
| CC | -1- SUBUNIT: HOMODIMER. | |
| CC | -1- SUBCELLULAR LOCATION: Secreted. | |
| CC | -1- TISSUE SPECIFICITY: IN MYCELA, AT A HIGHER LEVEL THAN LCL1, LCC2 | |
| CC | AND LCC3. | |
| CC | -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES. | |
| CC | -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS. | |
| CC | ----- | |
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| CC | modified and this statement is not removed. Usage by and for commercial | |
| CC | entities requires a license agreement (See http://www.isb-sib.ch/announce/ | |
| CC | or send an email to license@lsb-sib.ch). | |
| CC | ----- | |
| OR | EMBL: Z54277; CAA91042.1; - | |
| OR | InterPro: IPR001117; Cu-oxidase. | |


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QY 66 GPTLEADMGDTIOVTVINNNLETNGTSHHMGHLOKTNLHDGANGITECPPIPKGRKY 125
D 2 GPTLEADMGDMIOVTVINNNLETNGTSHHMGHLOKTNLHDGANGITECPPIPKGRKY 60
QY 126 REFKAQOYGTSMYHSHFSQOYNGVGAIOINGPASPDPDTDGVPPISYSSADELVE 185
D 61 TFOATQFGTSMYHSHFSQOYNGVGAIOINGPASPDPDTDGVPPISYSSADELVE 120
QY 186 LTKNS--CAPESDNYLFNGTAKHP--ETGESEYANVTLPGRHRLRLINTSEVNHFOVS 241
D 121 RIASHQAPRPSDNDGLNGSMWAPAGQTC--GKTTNTITAGKKYRLRLINTSEVNHFOVS 179
QY 242 LVNHTMCTIADMPVNAFVDSLFVGVQRYDVYIEANRTPGNTWENTYFEGGLCG-G 300
D 180 LDNHAFTVITSDFPVIVYTYANMIFIGIQRYDVYITLANQTVGSYWFRAEVONG--CGTN 237
QY 301 SRNPRAIIFHAGAPRPPDEGKAPVDHNCLEPRLKPVYARDV---PLEGFAKRADN 357
D 238 NNNNGIKISFTYSGAASPTSSA--TPYTGCTDEGTIIPWDSFVPSGSLSGNVEQLNV 296
QY 358 TLDVLTDTGTFPLFWKNGSAINIDMGRAVDYVLTONTSPFGYIYEVNGADQMSY 417
D 297 AINIGVDASG--PIYTWGINSALVDKPKPIQYVLDGNSMPASENLIELPNAQWY 355
QY 418 LIENDPG-----APFTLPHPMHLGHDFYVIGRSPDESASPNERHVEDPARDAGLLSGA 471
D 356 VIOEVPANVGNRPVSIINVPHPMLHGHDFELG----TGCVGTNNNTINGPSIDYD----- 406
QY 472 NPVRDYSMLPFGWVYLSFRADNPGAMLFCHIAMHVSGLGVY 517
D 407 NPTRDVAMLPAGMWVLAFTDNGCAMLHCHIAMHVSGLGVY 452

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RESULT 4

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QY 096WM9 PRELIMINARY; PRT: 581 AA.
AC 096WM9:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Laccase 2 (EC 1.10.3.2).
GN LCC2.
OS Botrytis cinerea (Botryotinia fuckelliana).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OC Helotiales; Sclerotiniaceae; Botryotinia.
OX NCBI_TaxID=40559;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SA556;
RA Schouten A., Vermeer J.E.M., van Kan J.A.L.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243855; AAK77953.1;
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOOPER_OXIDASE1; UNKNOWN_1.
DR PROSITE; PS00080; MULTICOOPER_OXIDASE2; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 581 AA: 63434 MW: 674947DAFD6BC757 CRC64;

```

Query Match 33.9%; Score 1071.5; DB 3; Length 581;
 Best Local Similarity 38.4%; Pred. No. 1.2e-69;
 Matches 220; Conservative 103; Mismatches 205; Indels 45; Gaps 17;

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QY 3 SC-NTPSNRACGTDGDIINTDYEVDSPDGVVRYTITLFEVDNMT-EGDGVVKEVMV 60
D 38 SCANATATRSKCGE--YSIDTMYDVTPNGVRETWLS--VENSTITPDGTYR-SAMTF 92
QY 61 NNSIGPTIFADMGDTIOVTVINNNLETNGTSHHMGHLOKTNLHDGANGITECPPIPKG 120
D 93 NOTVGPATITADMGDNLIHVTNNLNQHNCTSHHMGHROLDGSLGYGVGVGTCPIAP-G 151

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QY 121 GRKVRERKAQOYGTSMYHSHFSQOYNGVGAIOINGPASPDPDTDGVPPISDYSSA 180
D 152 DTLTYKFOATQYGTSMYHSHFSQOYNGVGAIOINGPASPDPDTDGVPPISDYSSA 211
QY 181 DELVELTKNSGAPESDNVLFNGTAKHP-----GGEYANVTLPGRHRLRLINT 232
D 212 FEIMDSARQAGAPALENTLMTNGTINIDCSASTDANCVGKKFELFVECTKRLRLIN 271
QY 233 SEVNHFOVSLVNHNTMCTIADMPVNAFVDSLFVGVQRYDVYIEANRTPGNTWENTY 292
D 272 GIDSHFEFLIDNHTLVIANDLVPIYPTDTLLIGIRYDVYIENAAADWYRLGN 331
QY 293 GGLCGSSRNYPYA-AIFHYAGAPRPPDEGKAPVDHNCLEP--NLKPVYARDVPS 349
D 332 --GTCSSSESAAMATGILRYSSTVDPSTVGTB--RGCADEPVASLVPHLATLV--G 386
QY 350 GFKA RADNLTDTTGTPLFWKNGSAINIDMGRAVDYVLTONTSPFGYIYEVNGADQ 409
D 387 GT-----SLVDEQVSPAFNTYFTWTNSSLIDWSSPTTLKIFENNETTLPDYVVALN 441
QY 410 GAD--QMSYWLIENTDGPFTLPHPMHLGHDFYVIGRSPDESASPNERHVEDPARDAG 466
D 442 QIDANEWVYVYIEDLTG--FGIMHPILHGHDFYVVAQETD-----VESATKSPA 490
QY 467 LLSGANPVRRDYSMLPFGWVYLSFRADNPGAMLFCHIAMHVSGLGVYLERADDLRG 526
D 491 NFNLVPPRRDVAALPFGNGCYLAIFKLDNPGSWLLCHIAMHVSGLGVYLERADDLRG 548
QY 527 AVSDADADDLDRICADWRRYTPNPKSDSG 559
D 549 AIGMSDTEIFEDTCANMNAITPELFAEDDSGI 581

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RESULT 5

```

QY 096WM9 PRELIMINARY; PRT: 561 AA.
AC 096WM9:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Laccase 1 (EC 1.10.3.2).
GN LCC1.
OS Botrytis cinerea (Botryotinia fuckelliana).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OC Helotiales; Sclerotiniaceae; Botryotinia.
OX NCBI_TaxID=40559;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SA556;
RA Schouten A., Vermeer J.E.M., van Kan J.A.L.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243854; AAK77952.1;
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOOPER_OXIDASE1; UNKNOWN_1.
DR PROSITE; PS00080; MULTICOOPER_OXIDASE2; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 561 AA: 60336 MW: 7F36B828EF73C23 CRC64;

```

Query Match 30.9%; Score 974.5; DB 3; Length 561;
 Best Local Similarity 36.9%; Pred. No. 1.2e-62;
 Matches 209; Conservative 82; Mismatches 229; Indels 47; Gaps 15;

```

QY 1 QOSC-NTPSNRACGTDGDIINTDYEVDSPDGVVRYTITLFEVDNMT-EGDGVVKEVMV 56
D 34 ROSCANATATRSKCGE--YASASTSYTYVTKGTSLVYVONTLS-----ADG-VSRP 82
QY 57 VMLNNSIGPTIFADMGDTIOVTVINNNLETNGTSHHMGHLOKTNLHDGANGITECP 116
D 83 TLNFGNCTIGPQITADMGDDVIVHTNKLTSNGTSHHMGHROLDNNAQYDGVGTCPI 142
QY 117 PRKGGRKYRERKAQOYGTSMYHSHFSQOYNGVGAIOINGPASPDPDTDGVPPISDY 176

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OY 125 YRFNAOQGTSMYSHSHSAOYGNQNVGAJQINGASLPYOTDLCGFPIISOYSSADELV 184
Db 165 YAFRTQJGIGTWHSHSHSLQABEFGMFIYFPTTANBYDEJLSTFLQDMWDGTAHGW 224
OY 185 ELTRNSGA-PESDNLVFNGT----AKHE----"GEGEYANVTLTPCRRLRLINISVE 235S
Db 225 DNVAASKGAGPLPANGLINGITWTFDOCKNSTDNCVGGKKESANFKKKHLIRINNSAD 284
OY 236 NHFOVSLVNHMCIADDMVYVNMATYDSLELGYGQRYDYIENKRPGRYWRVWTFGGG 295S
Db 285 AHFOPSIDGHLFYVANDLVPIKPFKTSYVSGORYDYIVEANAPRGWTLR----SG 340S
OY 296 LLC-----GGSNRPYPAIFHTAGAPGCPPTDEGKAPVDHCL--"DLENLKPVAYDPLS 349S
Db 341 MSCVPBGDGLARKRYVTGIRDKDSKADPKTSDVYVDFCSDEDPKKLYPLHALDVTH 400S
OY 350 GFAKRAADNTLDVTLDTTGTPL-----FYWKVNSAIIIDMGRAVYDYLQNTSFFPGYN 404S
Db 401 GEIYRS----"DlGKRPNGTPAEGONWRFQWTLNNSLVLVMDHPLERLIFGOSLFFPYDYN 456S
OY 405 IVEVNGADONGSYML-----ENDPGAPFTLPHPMHLHGDFVILGRSP----"DESP 451S
Db 457 YIKAD-CQLMWQAMVHTGDEQRPPTDPLRSHLAPRILHLHGDFVWLSQSRKAKWDGP 515S
OY 452 ASNERHVEDPARDAGLLSGANPVERDYSMLEPAFGVYVLSFRADNPAGMLEFHCHIAHWVG 511S
Db 516 RG-----FDI-----"KNPARDRDTAMLEPEKSHLAIARQLDNPGAMVLVHCHIAHWAG 561S
OY 512 GLGVYVLELRADDLGANSDDADDLRLCADMKRYKTYWTPNPKSDSL 559S
Db 562 GLSLFEVYSDP--"RIALGMPNHVDVFRQTCREKMDVARTKMPKPODSI 607S

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| RESULT | ID | Q8TFED9 | PRELIMINARY; | PRT; | 578 AA. |
|-----------------------|---|--|--------------------|------------------|-------------|
| 08TFED9 | AC | Q8TFED9; | | | |
| DT | 01-JUN-2002 | (TREMBLrel. 21, Created) | | | |
| DT | 01-JUN-2002 | (TREMBLrel. 21, Last sequence update) | | | |
| DT | 01-JUN-2002 | (TREMBLrel. 21, Last annotation update) | | | |
| DE | Laccase precursor (P1.10.3.2). | | | | |
| GN | LAC2. | | | | |
| OS | Gaeumannomyces graminis var. graminis. | | | | |
| OC | Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; | | | | |
| OC | Sordariomycetes; incertae sedis; Magnaporthaceae; Gaeumannomyces. | | | | |
| OX | NCBI_TaxID=36780; | | | | |
| RM | (1) | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RA | Lilvintseva A.P.; | | | | |
| RT | "Genetics of laccase in Gaeumannomyces graminis, the take-all | | | | |
| RT | fungus."; | | | | |
| RL | Thesis (2002), Department of Microbiology, | | | | |
| RL | Montana State University - Bozeman, Bozeman, USA. | | | | |
| DR | EMBL; AJ437320; CAD24842.1; - | | | | |
| KW | Signal; Oxidoreductase. | | | | |
| FT | SIGNAL | 1 | 15 | POTENTIAL. | |
| FT | CHAIN | 16 | 578 | POTENTIAL. | |
| SO | SEQUENCE | 578 AA; | 63650 MW; | 1A87EFA28742BD9C | CRC64; |
| Query Match | | 29.8%; | Score 940.5; | DB 3; | Length 578; |
| Best Local Similarity | | 36.0%; | Pred. No. 3.9e-60; | | |
| Matches | 205; | Conservative | 103; | Mismatches | 215; |
| | | | | Indels | 47; |
| | | | | Gaps | 21; |
| QY | 5 | NTPSRACWTCGYDINTDEV--DSPDTGVRRYTLETFEDVDMNTGPDGVYKREKMLVNN | 63 | | |
| Db | 41 | MTATRSQWCD-FDIKSDYTGQHPHTGTRFELTDSVK-LAPDVPR-YVQAFNCT | 97 | | |
| QY | 64 | ITGPTFADMGPTIOVTYNNL--ETNGSYIHMHGLKGTNMLHOGANGITECPJPKG | 121 | | |
| Db | 98 | VGPLVLMWMDGDDVYIHTYNNKLTQSLNGSYVMRHGLKQDQVLSDSQVSVTQCPSPV-CT | 156 | | |
| QY | 122 | KRYVFKAAQGYTSMYSHSFSAQYNGVGAIQINGPASPYPDTDGLVPISDIYYSSAD | 181 | | |

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Db 157 TQTKEFKATNPSSWYHSRHLAQMGVFGSGIITINGPASANTBEDGAMVYLSMGHKTPD 216
QY 182 ELVELTKNSGAPFSDNYLFGNTAKHPETGE--GEYANVTLTPGRHRRLRLINTSVENHQ 239
Db 217 ELMHQASQGPPLEMLNLINGMNYGAEAGNOTGRMWTSEACKSYRFLVNTAIDTHFR 276
QY 240 VSLVNHMCIITADMVVNMATYDSLEFLYGORTDYVTEANR--TGENTYFNTFGGGL 297
Db 277 FGJNHHTLVYIALDFIEVEPEYETTMVINGAGORVDYIVKADQAAVSDFLRALIPOSA-- 334
QY 298 CGG---SRNPYPALIEFYAGAPGSPRDEKAPDHNCIDLP--NLKPYVARDPVLSGFA 352
Db 335 CGTIEKMN--TRAIYHGSQGPST--TGHTYVD-ACEDEPLEKPKPIIRIDAEGSTY- 389
QY 353 KRAINTLDVTLDTTGTPLFENKVGASAINIDMGRAVVDYVLTONT--SEPPGYNIENGA 411
Db 390 ---EQKATATGANGVNGVFRKRYLINTSTMELDMDSNPYTSOLASNATYAFSNNAMVLEPA 446
QY 412 DQMSWYLIENDPGAFPTLPHPMHLGHDFYVLGSRPDESPASNERHVFDPARDAGILSGA 471
Db 447 DKMAYVLIQTD---FGVAHPILHGHDSYVLAQSGS-----AYQCG--VTKLITT 490
QY 472 NPVRDYSMLPAGFWYVLSFPADNPGAMLFCHTAMVYSGGLGVYTERADDL--KCAVS 529
Db 492 NPMRDRPAILPEAGHLVLAFTQDPNPGAMLHCHIGMTAOGFAPOFEVERSEMFSKNIIN 551
QY 530 DADADDRLCADRRRWYPTNPYKSSGL 559
Db 552 N---NDIEGLCEPWRTHVGKINIKLESGI 578

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[illegible]

| QY | 426 | FTPLP---- | HPMHLGHDEYVLGR----- | SPESPASNEHRHVEDPARDAGLLSGANPYRRD | 477 |
|-----------|--|---------------------------|--|----------------------------------|------------|
| | | | | | |
| Db | 476 | PRNLTPSRVPHLHHGHDPAILA | OGKGPPTPIAIFOLD----- | ----- | NPERRD 518 |
| QY | 478 | VSMPLAFGMYVLLSFRADNPGAMLF | FRCHLTAHWVSGLGVYLLERADDLRGAVSDADA--DDL | 536 | |
| | | | | | |
| Db | 519 | VVDVDIGGYAMIAFVENDRQAMLL | CHQGYHNASGMLAQYITEQSKIKPLIENAGVINDP | 578 | |
| QY | 537 | DLRLCADRRIRYPT----- | NPYKSSDGL 559 | | |
| | | | | | |
| Db | 579 | ENRCASMKRYRYNAVDPIDNPDRQD | DSGI 605 | | |
| RESULT 11 | | | | | |
| Q96DU0 | | | | | |
| ID | Q96DU0 | | PRELIMINARY; | PRT; | 436 AA. |
| AC | Q96DU0; | | | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Created) | | | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Last sequence update) | | | | |
| DT | 01-JUN-2002 (TREMBLrel. 21, Last annotation update) | | | | |
| DE | Potential laccase (Fragment). | | | | |
| OS | Fusarium proliferatum. | | | | |
| OC | Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; | | | | |
| OC | Hypocreales; Nectriaceae; Gibberella. | | | | |
| OX | NCBI_TaxID=42674; | | | | |

RA Kwon S.-I., van Dohn C.D., Anderson A.J.;
RT "Gene sequence analysis of an opportunistic wheat pathogen, an isolate
RT of *Fusarium proliferatum*.";
RL Can. J. Bot. 79:1115-1121(2001).
DR EMBL: AY008437; AAC623873.1; -
DR InterPro: IPR001117; Cu-oxidase.
DR Pfam: PF00394; Cu-oxidase; 3.
FT NON_TER 436 436
SQ SEQUENCE 436 AA; 45313 MW; 209AE8133485FEAA CRC64;

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 21.0%; | Score 662; | DB 3; | Length 436; |
| Best Local Similarity | 34.9%; | Pred. NO. 4.7e-40; | | |
| Matches 165; | Conservative 61; | Mismatches 149; | Indels 98; | Gaps 15; |

| | | | |
|----|-----|---|-----|
| QY | 91 | SIHHGJLHOKSTNLHDGANGTECEPIPPKGGKRYKRFKRAOQYGSWHSHFSQAOXGNYV | 150 |
| Db | 2 | SVHHGJLQRLQETFEEDDVGNGVTCQPIAP-GDSYTFTRAYOQGSWHSHSTSLQIADGDA | 60 |
| QY | 151 | GAIDINGPASIPLPYDIDLQVPEISDYSSADE--LVLEIFKNSGAPESDNLFGTKAKHBE | 208 |
| Db | 61 | GPITYGSSAPPEDEGRNPILITDMSHRSASQWRELVPNPNPRMKNGLVINGCNGFNG | 120 |
| QY | 209 | TGBEIYANVTITPBRRLRLINTSVENHQVLSLVNTHKCIITAADNYPVAAVTYDLSFLG | 268 |
| Db | 121 | SFPRERFMVYTKKAKYVLARINTSVDTMTFSDINNFMTSMSTDVPIOPYSVSHVLVLG | 180 |
| QY | 269 | VGQRYDVVITYEANRF-----PGNWFNVTFEGGGLCGSRNPYPALFIHYAAGGCP | 319 |
| Db | 181 | IGQRYHYILDANPNPTTKMPANRPGNTWYRTV--GAGCGCGFE-----PGNE | 225 |
| QY | 320 | PTDEGKAPVDHN-----CLD--LPMLKPVV-----ARDV | 346 |
| Db | 226 | P-DROGILRIYRNASSKLVPTTFERNYSLECRDEAYDELSPUYEMWVDKVIKNTYKSGOFI | 284 |
| QY | 347 | PLSGFAKRAQDTLAVTLDTGS-PELFYWKNGSAIINDMGRVAVDYVLQNTSFPPGYN- | 404 |
| Db | 285 | GLSKFAHREPELMDNFYMWAGCENPLMLNFESNPITLN-----KNTWNPDIYAV | 332 |
| QY | 405 | --IVEYNGADQWSYMLIENDPGAFPLP-----HPMHLGHDFYVLGRSPDESASPAN | 454 |
| Db | 333 | DLVYVPEDEKDKMYIATIPAPAPKTYKPNBAFAFVAPVAPHLHGHDFALLAQGNFSDL-- | 390 |
| QY | 455 | ERHVFDPARQGL--LSGANVPVRDVSQMLPAFGVNVLSFPADNPAGMLFPGHT | 505 |
| Db | 391 | -----DTGKYNLKFDPNPRDVLVLLPGLGGVLVAFAFADNGSMFLFCHT | 434 |

| RESULT | 12 | | | |
|--------|--|--------------|-----------|-------------------------|
| 096UP8 | | | | |
| ID | Q96UP8 | PRELIMINARY; | PRT; | 437 AA. |
| AC | Q96UP8; | | | |
| DT | 01-DEC-2001 (TReMBLrel. 19, Created) | | | |
| DT | 01-DEC-2001 (TReMBLrel. 19, last sequence update) | | | |
| DT | 01-JUN-2002 (TReMBLrel. 21, last annotation update) | | | |
| DE | Potential laccase (Fragment). | | | |
| OS | Fusarium proliferatum. | | | |
| OC | Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; | | | |
| OC | Hypocreales; Nectriaceae; Gibberella. | | | |
| OX | NCBI_TaxID=42674; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=NRRL 31071; | | | |
| RA | Kwon S.-I., van Dohn J.C.D., Anderson A.J.; | | | |
| RT | "Gene sequence analysis of an opportunistic wheat pathogen, an isolate | | | |
| RT | of <i>Fusarium proliferatum</i> ." | | | |
| RL | Can. J. Bot. 79:1115-1121(2001). | | | |
| DR | EMBL; AY008439; AA623875.1; - | | | |
| DR | InterPro; IPR001117; Cu-oxidase. | | | |
| DR | Pfam; PF00394; Cu-oxidase; 3. | | | |
| FT | NON_TER | 1 | 1 | |
| FT | NON_TER | 437 | 437 | |
| SO | SEQUENCE | 437 AA; | 49897 MW; | B14B154A35279061 CRC64; |

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 20.9%; | Score 661.5; | DB 3; | Length 437; |
| Best Local Similarity | 34.2%; | Pred. No. 5.1e-40; | | |
| Matches 159; | Conservative 70; | Mismatches 157; | Indels 79; | Gaps 16; |

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OY 11HHHGHOKCTNLHDDGANGTEPCPEPPKGRKYYRKAQOYGVSWYHSHFSYOQGVY 150
Dd 2 SIHHGHIGQNTMETMDGVNGTQCPPIAE-DTFFTERRALQIQGSWYHSHYSIQIADGIA 60
OY 151 GAIOIQINGPASPYPDITDLGVFPIISDYSSA--DELVELTERNSGAPESDNLFNGTAKHPE 208
Dd 61 GPITFGPSSAHYDEAKDPILITDMNHRSAFQEWERELTGVPTRPEKNSILMNGIGNFAG 120
OY 209 TGEGBYANVTITPGRRHLRLINTSVENHROYSLVNHTKCIITAAADYPVANAATVYDSIFLG 268
Dd 121 SEPRRRRYNTVTKKAKYLLRLINTSVTTFEFGIDNHYFEWMSDFVPIHRYVDHILWG 180
OY 269 VGORDDVYIEA---NRFP-----GNTWENTFEGGILGCGSRNPYPAALFHTAGAPCP 319
Dd 181 IGRKHVYLAHAKPRNDTFEPKPSDNGNTWIRVAAAG--CKGFED-----GN 224
OY 320 PTDEBKA-----PVD-----HNCLD--LPNLKEPVAVADYPLSGFARADNTLD 360
Dd 225 EPDEHOGILRYQPVSTEVPTQWRBDMNWKDCJDEKXYENLKPILPMSIPTVALDER-DRSKD 283
OY 361 VTLDT-----TGPLTFYKRWGSAIINDMGAADVYVLTONTSPSPCYINIVEYNGAD 412
Dd 284 LELGIEKVKDRPHAGDRFSWMAFGERPLMDFSNPTIT-LLEERKEWPDYVIVPAENRD 342
OY 413 QMSYWLINDGPAF-----TLPHMHMLHGDEYVLGSPDESPASNRHAYED 461
Dd 343 GMYVLVTI---AESLDIRIGTKNKTFRSLAHLEHLHGDFALLD-----GTNSSQIINDP 392
OY 462 ARDAGLLSGANPVRDYSMLPFAFGVWVLSFPRADNPAGMLFRCHIA 506
Dd 393 -NNPYTLKFDNPPRDVALIPAGGYLLVAFRADNPGSMLEFRCHIA 436
RESULT 13
O13448 PRELIMINARY; PRT; 520 AA.
AC O13448
AC O13448:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Laccase precursor (EC 1.10.3.2)

```

DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Laccase III (EC 1.10.3.2).
 OS Trametes versicolor (White-rot fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Trametes.
 OX NCBI_Taxid=5325;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schuren F.H.J., Friesenegger A., Hessing J.G.M., Schneider C.,
 RA van Mulijik G.M., Dezan M., van Zeyl C.M.J.,
 RA van den Hondel C.A.M.J., Pfaller R.,
 RT "Laccase production by genetic transformation of the basidiomycete
 RT Trametes versicolor."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY081188; AAL93622.1; -.
 KW Oxidoreductase.
 SQ SEQUENCE 520 AA; 55473 MW; E1147EC32317C632 CRC64;

Query Match 20.1%; Score 636; DB 3; Length 520;
 Best local Similarity 33.0%; Pred. No. 4,7e-38;

Matches 183; Conservative 70; Mismatches 207; Indels 94; Gaps 23;

QY 31 GVRPTLTLEVDNMTGPGVYKAYLNNSITIGPTIFADMGDTIQVTVINNLETN-- 88
 DB 24 GPVADLTITNAAY---SPGFSROAV-VVNGGTPPLITGCMGDRPOLANVINDLTNHTM 78
 QY 89 -GTSIHMHGKHOKTNGHANGITECPITPKGKRYRPFKA-QOYGTWYSHSFAOY 145
 DB 79 LKSTISHMHGFFQKGTWADGPAFINOCPI-SSGHSFLIDPQDAGTFWYHSHLSY 137
 QY 146 GNGVGAIOI---NGPASPYPDTDLG--VPEISDYYSADLVELTKNSGAPF---SDN 197
 DB 138 CCGLRGFEVYDPRDPAADYDVNDPTVITLADWYHVA-----KLGPAPPLGADA 189
 QY 198 VLENGTAKHETGEGEYANTLTGRRRLRLINTSVENHFQVSLVNHHTCIIADKVPV 257
 DB 190 TLINGKGRSPSTYADLVISVTPGKRYRFLVSLSCDPNHTFSIDGNMTIIFETDSINT 249
 QY 258 NAMTVDSLFGVGGORYVVEANRTPGNYMF--NVTGCGLLGGSNRPYPAIFHYGA 315
 DB 250 APLVYDSIQIFAAORISFVLEANOAVDNYMIRANPSFGNGFTGIN---SAILRIDGA 305
 QY 316 PGGPPTDEGRAPVDNCLDLPNLPVYARVPLSGFAKRADNTLDVLTGTPLFVWKV 375
 DB 306 AALEPTTQTSTPEP--LNEVNLHPLVATVPGSPVAGVDLATNMAFNENGTNPF--I 360
 QY 376 NSGAINIDMGRAVVDYVL-QONTIS--FPPG--YNIIVEYNGADQWSYWLIENTPGAPFTLP 430
 DB 361 NGASFPTPTVYVLIQIISGQNOADLLPSGSVSLPS-NADIEISFPATAAPGA---P 415
 QY 431 HPMHLGHDFYVYGRSPDESPASNERHVFDPADAG--ILSGANPVRRDY--SMLPAGF- 485
 DB 416 HPFHLGHAFVAVY-----KSGSTVYINYNPIFRDYVSTGTPAAGD 456
 QY 486 WYVLSFRADNPGAWLFRCHLTAHVSGIGVYVYLLBRADLRGAVSDADADDLRLCADWRR 545
 DB 457 NVYTRFRFTDNGPWFHLCHIDFHLFAGRAVYFAADIPDVASA----- 498
 QY 546 YWPTNPTPKSDSGL 559
 DB 499 ----NPVQAAMSDL 508

Search completed: December 4, 2002, 10:47:41
 Job time : 42 secs

GN CVL3.
OS Coriolus versicolor.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Coriolus.
OX NCBL_TaxID=57466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO30340;
RA Mikuni J.;
RN Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO30340;
RA Iimura Y.;
RN Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL: D13372; BAA22153.1; -
DR InterPro: IPR001117; Cu-oxidase.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1. 1.
KW Oxidoreductase; Signal.
FT SIGNAL 1 21
SQ SEQUENCE 520 AA; 55528 MW; F99429EAC9D71B0 CRC64;

Query Match 20.4%; Score 645; DB 3; Length 520;
Best Local Similarity 33.2%; Pred. No. 1e-38;
Matches 184; Conservative 70; Mismatches 206; Indels 94; Gaps 23;

QY 31 GVVAPYTLTLEVDNMTGPDGVVKEKVMVNSIIGPTIFADMGDTIQVTVINNLETN-- 88
DB 24 GPVADLTITNAAV-----SPGFSRQAV-VVNGGTPGLITGNMGRQANVINDLTHHTM 78
QY 89 --GTSIHMHGLHOKGTLHMGANGITECPTRPGKGRVYEFKA-QQGTSTYHSFSAQY 145
DB 79 LKSTSIHMHGFQFGTMMAGPAPINOCPI-SSGHSFLYDFQVDDAGTFYHSHLSTQY 137
QY 146 GNGVGAIOI---NGPASPFDLIG--VPEISDYSSADELVELTKNSGAPF---SDN 197
DB 138 CDGLRGPFVYDPRPADLDVNDOTVITLVDMYHAA-----KIGPAPFLGADA 189
QY 198 VLENGTAKHPEBTGGEYANVTLPGRHRRLINTSVENHFOVSLVNHMTCIIAADVPV 257
DB 190 TLINGKRSPTTADLSVTSVTPGKRYRFLVSLSDPNTFTSIDGHNMIIETDSINT 249
QY 258 NAMTVDSLEFLGCGRYDVIEANRTPGNWF--NVTGGGLCGGSRNPYPAIFHAGA 315
DB 250 APLVVDSDIQFPAORISFVEANQADVNTYIRANPNFGNGFTGIN---SAILRYDGA 305
QY 316 PGGPPTDEGKAPVDHNCIDLPNLKPVVARDVPLSGFAKRAADNTLDVTLDTTGTPLFV 375
DB 306 AAVEPTTQTTSTP-----LNEVNLHPLVATVAPGSPVAGVDLAINMAFNNGTNF-- 360
QY 376 NGASAINIDMGRAVVDYVL-TQNTS--PPPG--YNIIVEGADOMSTYLIENDGAPFLP 430
DB 361 NGASFPPTVYVLLQIISGAQMODLLPSGSVSLPS-NADIEISFPTAAAGA---P 415
QY 431 HPHMLHGHDEYVLRSPDESPPASNERHYFDPADAG--ILSGANPYRVDV--SMLPAG- 485
DB 416 HPHMLHGHAAVY-----KSAGSTVYNDPIFRDVSSTGTPAAG 436
QY 486 WVYLSFRADNPGAMLFCHIAMHVSGLGVYLLERADDLRGAVSDADADDRLCADMR 545
DB 457 NVYIRFTDNDGPMFLCHIDFHLGFAVFAEDIPDVASA----- 498
QY 546 WYPTNPYKSDSGL 559
DB 499 -----NPVQAWSDL 508

RESULT 14
ID 096UT7 PRELIMINARY; PRT; 520 AA.
AC 096UT7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Laccase B precursor (Ec 1.10.3.2).
GN LAC1.
OS Trametes versicolor (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBL_TaxID=5325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 32745;
RA Jolivalt C., Madzak C., Caminade E., Mougin C.;
RN "2,5-xylydine induced laccase from the basidiomycete Trametes
versicolor ATCC 32745.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF414109; AL07440.1; -
DR InterPro: IPR001117; Cu-oxidase.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
KW Oxidoreductase; Signal.
FT SIGNAL 1 21
SQ SEQUENCE 520 AA; 55576 MW; F3241CB929C247F9 CRC64;

Query Match 20.3%; Score 640; DB 3; Length 520;
Best Local Similarity 33.2%; Pred. No. 2.4e-38;
Matches 185; Conservative 69; Mismatches 203; Indels 100; Gaps 24;

QY 31 GVVAPYTLTLEVDNMTGPDGVVKEKVMVNSIIGPTIFADMGDTIQVTVINNLETN-- 88
DB 24 GPVADLTITNAAV-----SPGFSRQAV-VVNGGTPGLITGNMGRQANVINDLTHHTM 78
QY 89 --GTSIHMHGLHOKGTLHMGANGITECPTRPGKGRVYEFKA-QQGTSTYHSFSAQY 145
DB 79 LKSTSIHMHGFQFGTMMAGPAPINOCPI-SSGHSFLYDFQVDDAGTFYHSHLSTQY 137
QY 146 GNGVGAIOI---NGPASPFDLIG--VPEISDYSSADELVELTKNSGAPF---SDN 197
DB 138 CDGLRGPFVYDPRPADLDVNDOTVITLVDMYHAA-----KIGPAPFLGADA 189
QY 198 VLENGTAKHPEBTGGEYANVTLPGRHRRLINTSVENHFOVSLVNHMTCIIAADVPV 257
DB 190 TLINGKRSPTTADLSVTSVTPGKRYRFLVSLSDPNTFTSIDGHNMIIETDSINT 249
QY 258 NAMTVDSLEFLGCGRYDVIEANRTPGNWF--NVTGGGLCGGSRNPYPAIFHAGA 315
DB 250 APLVVDSDIQFPAORISFVEANQADVNTYIRANPNFGNGFTGIN---SAILRYDGA 305
QY 316 PGGPPT---DEGKAPVDHNCIDLPNLKPVVARDVPLSGFAKRAADNTLDVTLDTTGTPLFV 372
DB 306 AAVEPTTQTTSTP-----LNEVNLHPLVATVAPGSPVAGVDLAINMAFNNGTNF-- 359
QY 373 WKVNGSAINIDMGRAVVDYVL-TQNTS--PPPG--YNIIVEGADOMSTYLIENDGAPFLP 427
DB 360 --INGASFPPTVYVLLQIISGAQMODLLPSGSVSLPS-NADIEISFPTAAAGA-- 414
QY 428 TLPHMLHGHDEYVLRSPDESPPASNERHYFDPADAG--ILSGANPYRVDV--SMLPAG 483
DB 415 --PHPEHMLHGHAAVY-----KSAGSTVYNDPIFRDVSSTGTPA 453
QY 484 FG-WVYLSFRADNPGAMLFCHIAMHVSGLGVYLLERADDLRGAVSDADADDRLCAD 542
DB 454 AGDNVTIRFTDNDGPMFLCHIDFHLGFAVFAEDIPDVASA----- 498
QY 543 WYPTNPYKSDSGL 559
DB 499 -----NPVQAWSDL 508

RESULT 15
ID 08TFM1 PRELIMINARY; PRT; 520 AA.
AC 08TFM1;
DT 01-JUN-2002 (TReMBLrel. 21, Created)


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DB 143 A- GGLTLYKFPADNPGSSWYSHFLQYGDGLFGLVINGPATFANTVDVGLFLNDNM 201
OY 177 YSSADELVELTNGSGAPESDNVLENGTAKHPETGESEYANVTLPGRHRRLINTSVEN 236
DB 202 HVPVOSLIMKRAKTGAPPTLTGLMNGTNTY--NGACKKQOTFTPTPGIKYRIRVNTAVDG 259
OY 237 HVOVSLVNTMCIADAMPVNAATVDSLGLGVRDYVIEANRPNGYVNTVTEGGGL 296
DB 260 HPOFSTIDGSHFOYIADFPVIVPYNATSTLVSTAOXRIDITVYANAAVNTW--IRAGMOT 317
OY 297 LCGSHNRP-ALIFHYAGAPG-GPPTDEKAPVDHNCIDLPMIKRVPVARDVPLSGFAK 354
DB 318 ACGSNMNAINGILKRYTSSSTADPTTSTVASTSCDEP-----LASTVEFVPIPV 372
OY 355 ADNTLDVTLDTTGTPLFVKVNGSAINIDGRAVVDVYLTONTSPFGVIVENGADOM 414
DB 373 ASSIMKTTLTGGGQ--MLFNCSLLMWTDLTLVINSGNIMPTVEYVPIESTTAN 429
OY 415 STW--LIENDPGAPFTLPHMHLGHDFVYLGSRSPESPSNERNHVPDPARADGLISGAN 472
DB 430 KQMAVLAISGPNP--NHPIHLGHDFWTLSCGTGATYATP-----ALNLVN 474
OY 473 PVARDYSMLPAFGVYVLSFRADNPGAMLEFCHITAMHVSGLGVYTLERADLNGAVSDAD 532
DB 475 PPRROVWTLPTGSHLVIAFOIONPGSMLMCHIAMHASEGLAQVESESSILPTGTAD 534
OY 533 ADDDLRLCADMRIRYPTNPEPKSDSGI 559
DB 535 VSTFQNTCAAMKAWPTPEPPDDSGI 561

RESULT 6
O8TFE4 PRELIMINARY: PRT: 608 AA.
AC O8TFE4;
DT 01-JUN-2002 (TREMBLREL. 21, Created)
DT 01-JUN-2002 (TREMBLREL. 21, last sequence update)
DT 01-JUN-2002 (TREMBLREL. 21, last annotation update)
DE Laccase precursor (EC 1.10.3.2).
GN LAC1.
OS Gaemannomyces graminis var. tritici.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes Incertae sedis; Magnaporthaceae; Gaemannomyces.
OX NCBI_TaxID-36779;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21861250; PubMed-11872481;
RA Litvinseva A.P.; Henson J.M.;
RT "Cloning, characterization, and transcription of three laccase genes
RT from Gaemannomyces graminis var. tritici, the take-all fungus.";
RL Appl. Environ. Microbiol. 68:1305-1311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Litvinseva A.P.;
RT "Genetics of laccase in Gaemannomyces graminis, the Take-All
RT fungus.";
RL Thesis (2002), Department of Microbiology,
RL Montana State University-Bozeman, Bozeman, USA.
DR EMBL: AJ417685; CAD10747.1; -.
KW Signal; Oxidoreductase.
FT SIGNAL 1 18
FT CHAIN 1 18
SQ SEQUENCE 608 AA; 67421 MW; 094F7852FAA602F0 CRC64;

Query Match 30.2%; Score 954; DB 3; Length 608;
Best Local Similarity 35.5%; Pred. No. 4.3e-61;
Matches 209; Conservative 94; Mismatches 223; Indels 62; Gaps 17;
OY 5 NPSNRACWTDGYDINTDYVSDPTGVVPRYTLTLEVDNMTGPDGVVEKVALVNSI 64
DB 50 NGRKSRNCW-GKSIDINNYETAPDVTREYMLSVBE--GICNNDG-YKRYCOTFNGSF 105
OY 65 IGPPIFADMDGTIOVYINNLLETNGTSHHGHGKQCTNLHDGANGITECPPIPKGRKY 124

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DB 106 PGPLIANNMGDNLVHYVTNNMKTNGTALHHGHGKQSVEXDSDPVCOTCIAP-GKSLT 164
OY 125 YRFKAQOYGTSWYSHFSAOYGVNGVGAIOINGPASPILPTDGLVPIISDYSSADELY 184
DB 165 YKFRVYQYGTWYHSHFSLQYTGELGPMIFGYPTTANVEDEDGTLFDMDHDTAMHG 224
OY 185 ELTKNSGA-PESDNVLENG-----AKHPET-----GGGEYANVTLPGRHRRLINTSV 235
DB 225 ENVASGAGPLPANGLINGNTFDCKNSTDTNCLGGKFSATFKKAKHLININSAD 284
OY 236 NHOVSLVNTMCIADAMPVNAATVDSLGLGVRDYVIEANRPNGYVNTVTEGGG 295
DB 285 AHQFSTIDGSHFLVNSDVLPIKFKTQSVRSVIGRQDYIVANAKPGDYMLR-----SG 340
OY 296 LLC-----GGRNPYPAIFHYAGAPGPPDEKAPVDHNCI--DLNLRVPVARDVPLS 349
DB 341 MSCVPEDTGALRRRYVGIIRYDKRSKADPKTSDVYVDETCSDDEPKKLPVHALDYTHM 400
OY 350 GFAKBRADNTLDVTLDTTGPPL-----FVKVNGSAINIDGRAVVDVYLTONTSPFGYN 404
DB 401 GEIVQS-----DLGFKPNGTPABEQNMFOVTLNSSLVDLHDHPTLETIPDROSIFPTKIN 456
OY 405 IVEVN-----GADQWSYLIEND-----PGAPFTLPHMHLGHDFVYLGSRP--DESP 451
DB 457 VIAEPATAPASKWTLVYIOSNEILLTLPSSHSTPHILHGHDFWVLSQSAKMDGTP 516
OY 452 ASNERHVPDPARADGLISGANPVARDYSMLPARGVYVLSFRADNPGAMLEFCHITAMHVS 511
DB 517 RG-----FNTKNPARBDTAMLPAGGHIAIAQOLDNPGMVLHCHIAMHAG 562
OY 512 GLGVYTLERADDLRGAVSDADADDLRLCADMRIRYPTNPEPKSDSGI 559
DB 563 GLSEFVESQG--RIALGMPDHHVFOQTCREMDAVRNKMPFPQDSDGI 608

RESULT 7
O8TFE1 PRELIMINARY: PRT: 607 AA.
AC O8TFE1;
DT 01-JUN-2002 (TREMBLREL. 21, Created)
DT 01-JUN-2002 (TREMBLREL. 21, last sequence update)
DT 01-JUN-2002 (TREMBLREL. 21, last annotation update)
DE Laccase precursor (EC 1.10.3.2).
GN LAC1.
OS Gaemannomyces graminis var. graminis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes.
OC Sordariomycetes Incertae sedis; Magnaporthaceae; Gaemannomyces.
OX NCBI_TaxID-36780;
RN [1]
RP SEQUENCE FROM N.A.
RA Litvinseva A.P.;
RT "Genetics of laccase in Gaemannomyces graminis, the take-all
RT fungus.";
RL Thesis (2002), Department of Microbiology,
RL Montana State University-Bozeman, Bozeman, USA.
DR EMBL: AJ437319; CAD24841.1; -.
KW Signal; Oxidoreductase.
FT SIGNAL 1 18
FT CHAIN 1 18
SQ SEQUENCE 607 AA; 67595 MW; 908C01BC3E2AD7F CRC64;

Query Match 30.2%; Score 953.5; DB 3; Length 607;
Best Local Similarity 35.9%; Pred. No. 4.7e-61;
Matches 211; Conservative 87; Mismatches 227; Indels 63; Gaps 18;
OY 5 NPSNRACWTDGYDINTDYVSDPTGVVPRYTLTLEVDNMTGPDGVVEKVALVNSI 64
DB 50 NGRKSRNCW-GKSIDINNYETAPDVTREYMLSVBE--GICNNDG-YKRYCOTFNGSF 105
OY 65 IGPPIFADMDGTIOVYINNLLETNGTSHHGHGKQCTNLHDGANGITECPPIPKGRKY 124
DB 106 PGPLIANNMGDNLVHYVTNNMKTNGTSHHGHGKQSVEXDSDPVCOTCIAP-GKSLT 164

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| | | | |
|----|-----|---|-----|
| QY | 82 | INNETNCTSIHHMGJHOKGNGLDANGANGTEECIPKRGKRYKRYRFAAQOYGSWHSHE | 141 |
| Dd | 106 | TNRLRTNCTSIHHMGVGRKLNKNNPMDGANGITECIPRNAS-KYRFRVEDYGTAMVHSHE | 164 |
| QY | 142 | SAOTGNGVYCAIQTNGPASPDPYTDLCGFVPISDYIYSADAEL-VELTKNSGA-PFSDNVL | 199 |
| Dd | 165 | SGOYGNGVYGLTFLENGPASPDPYQEDDLGVYPTDMYURGADEIOLFSLIPSPGVPPSPDNL | 224 |
| QY | 200 | FNGTAKHPETEGEYEVANTLTPGRHRHLRLNTSVENHPOVSLYVNHMCJIAADWYVNA | 259 |
| Dd | 225 | FNQSVYVNAQ-OGGGSYNRKYLKPGRRHLRLRIINTSVDTFTFVYSLYGHOFYIQTDFEYVNA | 283 |
| QY | 260 | MTVDLSELFVGWQRYDYVYIEANRTPGMYWNTFEGGGLICGSRNPYPAIFHYAGAPG-C | 318 |
| Dd | 284 | FTTSQIFLFGIGORQYDVYIEANQPGNDWFMFNTFASGLCTSLQKPAISIFOYEGASDPA | 343 |
| QY | 319 | PRTEGKARVDNHCNLDLBNLKVYARVDYVPSGFAKRNADLDYTDL---TGPRFLPVWK | 375 |
| Dd | 344 | LPTNGPPTPTSLCEDLMSWTVPYAKNVPRAFSAGVNTLEANTYENNEGGRORYWEI | 403 |
| QY | 376 | NGSAINIDMGREAVVDYVLTQNTSPPEPGYNIYEVNGADOMSWYLENDPGAFPTLPHPHML | 435 |
| Dd | 404 | NGSDONTYIMDEPTLETLEYLKVGMNPNFNNVYQVPOQNMSPWITQN---PTVAPHPHML | 459 |
| QY | 436 | HGHDFYVLGRSPDE-SPASNENRHYFPDPARADGLLSGANPVRQVYSMLPARGVYLSHRAD | 494 |
| Dd | 460 | HGHDFYLLGRSPADQTNPPAGVPRRBNATDYLATLRFDPNPAKRDVTMLPANGMWLVAPRTD | 519 |
| QY | 495 | NGGAWLFFCHIAVMHYSGGILGVVYLERADDLGAVASDADADDLRLCAADMRRYPTNYPK | 554 |
| Dd | 520 | NGGAWLFFCHIAVMHVAQGLSVQFLERQODIPSAP---PLSAIEPTCSQMTAYATSPHQ | 576 |
| QY | 555 | SDSGL 559 | |
| Dd | 577 | HDSEGL 581 | |

| RESULT 2 | ID | 09CA97 | PRELIMINARY: | PRT: | 589 AA. |
|-----------------------|--|---|-----------------|-------------|---------|
| AC | 09CA97: | | | | |
| DT | 01-JUN-2001 | (TREMBLrel. 17, Created) | | | |
| DT | 01-JUN-2001 | (TREMBLrel. 17, Last sequence update) | | | |
| DT | 01-JUN-2002 | (TREMBLrel. 21, Last annotation update) | | | |
| DE | Laccase. | | | | |
| GN | LACI. | | | | |
| OS | Glomerella lagenarium (Anthracnose fungus) (Colletotrichum lagenarium). | | | | |
| OC | Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes Incertae sedis; Phyllachorales; Phyllachoraceae; OC | | | | |
| OC | mitosporic Phyllachoraceae; Colletotrichum. | | | | |
| OX | NCBI_TaxID=5462; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=104-T; | | | | |
| RA | Tsui G., Fujikawa J., Ishisa H., Horino O., Kubo Y., RT | | | | |
| RT | Laccase gene LACI of Colletotrichum lagenarium is not essential for RT | | | | |
| RL | melanin biosynthesis and pathogenicity."; | | | | |
| RL | Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases. | | | | |
| DR | EMBL: AB055709; BAB32575.1; - | | | | |
| DR | InterPro: IPR001117; Cu-oxidase. | | | | |
| DR | InterPro: IPR002355; MulticCu_oxidase2. | | | | |
| DR | InterPro: IPR001854; Ribosomal_L29. | | | | |
| DR | Pfam: PF00394; Cu-oxidase; 3. | | | | |
| DR | PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1. | | | | |
| DR | PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1. | | | | |
| DR | PROSITE: PS00579; RIBOSOMAL_L29; UNKNOWN.1. | | | | |
| SO | SEQUENCE 589 AA; 64652 MW; B20692456A3F8E1 CRC64; | | | | |
| Query Match | 46.3%; | Score 1461.5; | DB 3; | Length 589; | |
| Best Local Similarity | 50.3%; | Pred. No. 5e-98; | | | |
| Matches 285; | Conservative | 84; | Mismatches 175; | Indels | 23; |
| | | | | | Gaps 13 |

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0Y      3 SCNT--PSNRACWTDGDINDINDYVDSPDGVAPRYTLTLEVDNMGPRGVAKEMVL 60
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      36 SCGHGPRNRCACMGNDINSDYETSPSTGCRVYDFITTNVDFAA-DEISK-PMALI 93
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y      61 NNSIIGPTIFADMGDTIOVTVINNLETNGTSHMHGHLQKGTMLHDGANGITECRLPKG 120
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      94 NGGPRGPTIFEADMGDWEIYNHNOADNGTSHHGHGHSNRSDOANGCANGTECRLP-G 152
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y      121 GRKYRFRFAOQYGTSMWHSHESAOYGNGVGAIOINGRPASLPYDTDLGVPISDYUSSA 160
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      153 HSKRYKRFEMIDYGTSMWHSHESSOYGGNGVGAIKINGPASADYDIDLGPTVSDWYDFA 212
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y      181 DEL---VELTKNSCAPSDNVLNGTKAKHPTGSGEYANTLTPGRBHRRLINTSVENH 237
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      213 DRLERQALVANGPPDSDNVLENGTINMAO-GGGQYSKTKLTPGKKHRLINPSVDNT 271
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y      238 FOVSLVNTMCLILADMPVNAKAVDSLSFLGQGRYUVYVEANKRPNMYFNVTFCGGGL 297
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      272 FTVSLVNGHSFLVAFDLVPKPVYKDSLFSVQGRYVITLHADVDGNTMYFNMTLASGL 331
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y      298 CGGSRNPYPALIFHYAGAGGPRPDEGKAPVDNCLDLPLKPYVAVADVPLSGFAKADN 357
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      332 CGTSMKRPASIFTEYGADLPLEEGGVPA-ADCVDTGSPYLAHAAPEAEETPN-KN 389
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y      358 TLDVLTDT---GPRPLVWKYNGSAINIMDCRAVADVLTQNTSFPBGVNIYVENGSDOM 414
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      390 TLDVLEQPEIHGEIKYRWKNGSSMDOMKPTLQYTLABGNSDMPOAHNVYDLSGADV 449
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y      415 SYMLIENDPGAPFTLPHPMHLHGHDYFLGRSPDESPASNERHYFDPDARAGL--TSGAN 472
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      450 TMMVYV-TGA---LPHHILHGHDFLLGLGDGRKFSSNSTNGTGYSSVXYPSLAFAN 505
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y      473 PVRDYSMLPAFGVYVLSFRAHDPGAWLFECHIAHMYSGLGUYVLERADDLRGAVSDAD 532
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      506 PTRRDYVADLPNGMVVIAFETDNGAMILHCHIAHWSMGLSYOFIERKEDEITSALK--- 562
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y      533 ADDLDRLCADMRRYTPNYPKPSGL 559
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      563 LETTLDQCTQWKDYAHAAFPKIDSGL 589
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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| RESULT 3 | | | |
|----------|--|--------------|-------------------------|
| ID | 0960M2 | PRELIMINARY: | PRT: 454 AA. |
| AC | 0960M2: | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Created) | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Last sequence update) | | |
| DT | 01-MAR-2002 (TREMBLrel. 20, Last annotation update) | | |
| DE | laccase (EC 1.10.3.2) (Fragment). | | |
| CN | LCG3 | | |
| OS | Botrytis cinerea (Botryotinia fuckelliana). | | |
| OC | Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; | | |
| OC | Helotiales; Sclerotiniaceae; Botryotinia. | | |
| OX | NCBI_TaxID=40559; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Schouten A., Deloy S., van Kan J.A.L.; | | |
| RL | Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases. | | |
| DR | EMBL; AY047482; AAL06114.1; - | | |
| DR | InterPro; IPR001117; Cu-oxidase. | | |
| DR | InterPro; IPR002355; MulticU_oxidase2. | | |
| DR | Pfam; PF00394; Cu-oxidase; 3. | | |
| DR | PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1. | | |
| DR | PROSITE; PS00080; MULTICOPPER_OXIDASE2; UNKNOWN_1. | | |
| KW | Oxidoreductase. | | |
| FT | NON_TER | 1 | |
| FT | NON_TER | 454 | |
| SQ | SEQUENCE | 454 AA; | EB56A720394D912A CRC64; |

| Query Match | | | |
|---------------------------|-------|-----------------|--------------------|
| Best Local Similarity | 47.2% | Score 1113.5; | DB: 3; Length 454; |
| Matches 220; Conservative | 72; | Mismatches 145; | Indels 29; Gaps 12 |

DR InterPro: IPR002355; MultiCu_oxidase2.
 DR Pfam: PF00394; Cu-oxidase; 3.
 DR PROSITE: PS00079; MULTICOPPER OXIDASE1; FALSE NEG.
 DR PROSITE: PS00080; MULTICOPPER OXIDASE2; FALSE NEG.
 KM Oxidoreductase: Signal; Copper; Metal-binding; Glycoprotein; Repeat;
 KW Lignin degradation; Multigene family; Polymorphism.
 FT SIGNAL 1 19
 FT CHAIN 20 531
 FT DOMAIN 23 146
 FT DOMAIN 158 315
 FT DOMAIN 384 507
 FT METAL 83 83
 FT METAL 85 85
 FT METAL 128 128
 FT METAL 130 130
 FT METAL 427 427
 FT METAL 430 430
 FT METAL 432 432
 FT METAL 479 479
 FT METAL 480 480
 FT METAL 481 481
 FT METAL 484 484
 FT METAL ? ?
 FT CARBOHYD 66 66
 FT CARBOHYD 109 109
 FT CARBOHYD 186 186
 FT CARBOHYD 231 231
 FT CARBOHYD 280 280
 FT CARBOHYD 395 395
 FT VARIANT 42 42
 FT VARIANT 119 119
 FT VARIANT 246 246
 FT VARIANT 256 256
 FT VARIANT 261 261
 SO SEQUENCE 531 AA; 57545 MW; 737339803F75AB19 CRC64;

Query Match 17.9%; Score 564; DB 1; Length 531;
 Best Local Similarity 30.8%; Pred. No. 7.9e-33;
 Matches 174; Conservative 62; Mismatches 171; Indels 158; Gaps 27;

QY 25 VDSPTGVNRYPTLTLEVDNMTGPDGVNKEKVLVNNSTIGPTIFADMGDTQVYINN 84
 DB 14 VSTPAPAANRKRKEDINNVN--VAPDG-FQRPVSVNGLVPGTLLTANKGDTLRINVTNQ 70
 QY 85 LE---TNGTSIHWHGLOKGTNLHDGANGTECPRPKGGKRYRKAQ---OYGTSMY 137
 DB 71 LTDPMSMRATTIHHGGLFQATLADDEGPAFYTCPI---AQNLSYIEIPLHGOTIMY 127
 QY 138 HSHPSAIOYGNGVGAIOI---NGPASPYPDT--LGVFPISDYYSADAEV--LTKN 189
 DB 128 HAHLASQYVGLNGPLVIYDPNDPHKSRDYDDASTVVMLEDMYHTPAVLEKQMFSTNN 187
 QY 190 SG--APFSQNVLENGTAKHPETGEGEYANTLTP-----GRRHRLRLINTSVENHFQ 239
 DB 188 TALSPVPDGLN-----GGRYVGGPAPVRSYINVRGRKRYRLRVINASAGISFT 239
 QY 240 VSLVNHMTCLIAADMEVNMATVDSLFGVQORYVYIEANRTPGNMYFN--VTFGGGLL 297
 DB 240 FSIEGHRLTYIADGIRPHQPLPYDSFOIYAGORSYIVTEANQTAANWIRAPMTVAG--- 296
 QY 298 CGGSRNTPA---AIFHYAGAPGCPPTDE-----GKAPVDHNCIDLPLKRVVARDVPLS 349
 DB 297 AGTNANLDPNVPVAVLHYEGAPNAEPTEEGSAIGTALVEENLHALIN----- 344
 QY 350 GFAKRAUNDTLDTLTGTPLFVWKGSA-----INIDMGRAVVDVLT-----ON 396
 DB 345 -----PGAP-----GGSAPADVSLNLAIGRSTYVDSILKFTFNNTKYE 382
 QY 397 TSPPPGTIVEVNGADQWSTWLIENDPAPPT-----LP-----HPMHL 435
 DB 383 PSLEPTLLKILANNAS-----ND--ADFTPNEHTIVLPNNKVIGAQHHRGADPHIL 431
 QY 436 GHGDFYV---LGRSPDPSAPSNRHHVDPARDAQLLSGANVVRDVSMLPAFGWVLSFR 492

DB 432 GHGFDIVKSLGCTPNY-----VNPRRDVRVGCTG-VLIRFK 469
 QY 493 ADNPGANLFRCHT--AMHVSGLGV 515
 DB 470 ADNPGPWFHCHIDCTWRIGSHLSL 494

Search completed: December 4, 2002, 10:45:37
 Job time: 16 secs

DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Laccase 2 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
 DE (Urishiol oxidase) (Diphenol oxidase) (Laccase I).
 GN LCC2 OR LCC1.
 OS Trimetes versicolor (White-rot fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphelipholales; Trimetes.
 OX NCBI_Taxid=5325;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=52J;
 RX MEDLINE=97464057; PubMed=9322748;
 RA Ong E., Pollock W.B., Smith M.;
 RT Cloning and sequence analysis of two laccase complementary DNAs from
 RT the ligninolytic basidiomycete Trimetes versicolor.*;
 RL Gene 196:113-119(1997).
 CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
 CC PRODUCTS (PROBABLE).
 CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzenesemiquinone + 2
 CC H(2)O.
 CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
 CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
 CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
 CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL: U44851; AAA86659.1; -
 DR EMBL: U44430; AAC49828.1; -
 DR HSSP: P37064; IAO2.
 DR InterPro: IPR001117; Cu-oxidase.
 DR Pfam: PF00394; Cu-oxidase; 3.
 DR PROSITE: PS00079; MULTICOPPER_OXIDASE2; FALSE NEG.
 DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; FALSE NEG.
 KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
 KW Lignin degradation; Multigene family.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 1 519 LACCASE 2.
 FT DOMAIN 22 147 PLASTOCYANIN-LIKE 1.
 FT DOMAIN 159 301 PLASTOCYANIN-LIKE 2.
 FT DOMAIN 368 490 PLASTOCYANIN-LIKE 3.
 FT METAL 84 84 COPPER (TYPE 2) (BY SIMILARITY).
 FT METAL 86 86 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 129 129 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 131 131 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 415 415 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 418 418 COPPER (TYPE 2) (BY SIMILARITY).
 FT METAL 420 420 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 472 472 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 473 473 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 474 474 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 478 478 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 69 69 D -> V (IN REF. 1; AAC49828).
 SQ SEQUENCE 519 AA; 55810 MW; BFF5B4CD007702 CRC64;

Query Match 18.0%; Score 570; DB 1; Length 519;
 Best Local Similarity 29.9%; Pred. No. 2,9e-33;
 Matches 163; Conservative 73; Mismatches 201; Indels 108; Gaps 22;
 OY 49 PDGVAKKVMVNNNSITGPIIFADMGCTIOY----TYNNLENGNSIHHGHQKNTL 104
 DB 37 PDGFLRDAI-VVNGVVPSPILITGKGRFQIANDDTLTNNMKLSIHHHGEFOACTNW 95
 OY 105 HDGANGITECPPIPKGGRKRYRFKA--OQYGSWYHSFHSOYGVGVALOI--NGPAS 160
 DB 96 ADGPAFVNOCPI-ASGHSFLYDFHVPDQAGTFWYHSLSIQCDGLGPRVYVDKPRPA 154
 OY 161 LPYTD--LGVFPISDYYSADDELVELTKNSGAPF---SDNYLENGTAKHPETEGEYA 215
 DB 155 SRVDVNESIVITLDMYHFAA-----RLGPRFLGADATLNLGHSASTPAA 206
 OY 216 MYLTPRRRLRLINISVENHFOYSLVNTKCIADAMPVNAWYDLSFLVGGRYD 275
 DB 207 VINVQHGKRRYRFLVYSICDPNTFTSIDGNTLVYIEVDGINSOPLVDISQIFAORYSF 266
 OY 276 VIEANRTPGVWYF--NVTFCGGLICGSRNPDYPAIRFVAGAPGPTDEGKAPVDHNC 333
 DB 267 VLNANQVGNVWYRANRFTGVGAGIN-----SAILRQGARVAEFTTQTTSV----- 317
 OY 334 DLP---NLKPVYADVPLSGFAKRADNTLDVLTDTTGPLFWKVGSA-----I 380
 DB 318 -PLIETNLPLARMVPVSGPTPGVDKALNLFNFGNTNF--INNATPTPTVPL 373
 OY 381 NIDMGRAVVDVYLTONSF--PGNIVEVNGADOMSWLENDPGAFPLRPHNLGHND 439
 DB 374 QILSGAQTADLLPAGSVYPLPAHSTET-----TLPAFALAGA---PHEPHLGH 423
 OY 440 FVYLGSRSPDESASNERHVPDPADAG--LLSGANPRRDY--SMLPAGF-WVYLSRAD 494
 DB 424 FAYV-----RSGSTTYNNNDPIFRQVYSGTPAADNTYIRQTD 464
 OY 495 NPGAMLFCHIAHVSGLGVTLIERADIRGAVSDADDDRLCADMRRYWFTNYPK 554
 DB 465 NPGWFLHCHIDFLDGAIVFAEDVADVKAA-----NVPK 502
 OY 555 SDGSL 559
 DB 503 AMSDL 507
 RESULT 14
 LACC3.THACU STANDARD; PRT; 572 AA.
 AC 002079;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Laccase 3 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
 DE (Urishiol oxidase) (diphenol oxidase).
 GN LCC3.
 OS Thanaeophorus cucumeris (Black scurf of potato) (Rhizoctonia solani).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Heterobasidiomycetidae; Ceratobasidiatales; Ceratobasidiaceae;
 OC mitosporic Ceratobasidiaceae; Rhizoctonia.
 OX NCBI_Taxid=107832;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NS22;
 RX MEDLINE=96171523; PubMed=8598061;
 RA Wahlthier J.A., Xu F., Brown K.M., Brown S.H., Gollightly E.J.,
 RA Halkier T., Kauppinen S., Pederson A., Schneider P.;
 RT "The identification and characterization of four laccases from the
 RT plant pathogenic fungus Rhizoctonia solani.*";
 RL Curr. Genet. 29:395-403(1996).
 CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
 CC PRODUCTS (PROBABLE).
 CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzenesemiquinone + 2
 CC H(2)O.

Query Match Best Local Similarity 19.1%; Score 603; DB 1; Length 520; Pred. No. 1,3e-35; Matches 180; Conservative 76; Mismatches 211; Indels 92; Gaps 24;

Sequence 520 AA; 55643 MW; 16469DC547C61P3C CR664;

Query Match Best Local Similarity 19.1%; Score 603; DB 1; Length 520; Pred. No. 1,3e-35; Matches 180; Conservative 76; Mismatches 211; Indels 92; Gaps 24;

Sequence 520 AA; 55643 MW; 16469DC547C61P3C CR664;

Query Match Best Local Similarity 19.1%; Score 603; DB 1; Length 520; Pred. No. 1,3e-35; Matches 180; Conservative 76; Mismatches 211; Indels 92; Gaps 24;

Sequence 520 AA; 55643 MW; 16469DC547C61P3C CR664;

| | |
|------|--|
| CC | ApHyphlophares; Trametes. |
| OX | NCBI_TaxID=47662; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | TISSUE-Mycellium; |
| RX | MEDLINE-97076915; PubMed-8975613; |
| RA | Javer D.S., Xu F., Golightly E.J., Brown K.M., Brown S.H., |
| RA | Rey M.W., Schneider P., Halkier T., Mondorf K., Dallogg H.; |
| RT | "Purification, characterization, molecular cloning, and expression of two laccase genes from the white rot basidiomycete trametes villosa."; |
| RL | Appl. Environ. Microbiol. 62:834-841(1996). |
| CC | -I- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED PRODUCTS (PROBABLE). |
| CC | -I- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2 H(2)O. |
| CC | -I- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY). |
| CC | -I- SUBUNIT: HOMODIMER. |
| CC | -I- SUBCELLULAR LOCATION: Secreted. |
| CC | -I- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOOPER OXIDASES. |
| CC | -I- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS. |
| CC | ----- |
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| CC | ----- |
| DR | EMBL; LA9376; AAC41686.1; . |
| DR | HSSP; P37064; IAOZ. |
| DR | InterPro: IPRO00117; Cu-oxidase. |
| DR | InterPro: IPRO02355; Multicu_oxlase2. |
| PFam | Pf00394; Cu-oxidase; 3. |
| DR | PROSITE; PS00079; MULTICOOPER_OXDASE1; 1. |
| DR | PROSITE; PS00080; MULTICOOPER_OXDASE2; FALSE NEG. |
| KW | Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat; Lignin degradation; Multigene family. |
| KW | Lignin degradation; Multigene family. |
| FT | SIGNAL 1 21 POTENTIAL. |
| FT | CHAIN 22 520 LACCASE 1. |
| FT | DOMAIN 23 148 PLASTOCYANIN-LIKE 1. |
| FT | DOMAIN 160 302 PLASTOCYANIN-LIKE 2. |
| FT | DOMAIN 369 491 PLASTOCYANIN-LIKE 3. |
| FT | METAL 85 85 COPPER (TYPE 2) (BY SIMILARITY). |
| FT | METAL 87 87 COPPER (TYPE 3) (BY SIMILARITY). |
| FT | METAL 130 130 COPPER (TYPE 1) (BY SIMILARITY). |
| FT | METAL 132 132 COPPER (TYPE 3) (BY SIMILARITY). |
| FT | METAL 146 416 COPPER (TYPE 1) (BY SIMILARITY). |
| FT | METAL 419 419 COPPER (TYPE 2) (BY SIMILARITY). |
| FT | METAL 421 421 COPPER (TYPE 3) (BY SIMILARITY). |
| FT | METAL 473 473 COPPER (TYPE 3) (BY SIMILARITY). |
| FT | METAL 474 474 COPPER (TYPE 1) (BY SIMILARITY). |
| FT | METAL 475 475 COPPER (TYPE 3) (BY SIMILARITY). |
| FT | METAL 479 479 COPPER (TYPE 1) (BY SIMILARITY). |
| FT | METAL ? ? COPPER (TYPE 1) (BY SIMILARITY). |
| FT | CARBOND 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOND 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOND 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOND 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOND 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOND 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOND 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL). |
| SQ | SEQUENCE 520 AA; 55545 MW; 046ABDD7473/C6DE CRC64; |

Query Match 20.1%; Score 636; DB 1; Length 520;
 Best Local Similarity 33.0%; Pred. No. 5.8e-38;
 Matches 184; Conservative 69; Indels 100; Gaps 24;

```

Db      24 GPVADLFTTNAAY-----SPDEFSQAV-YVNGGTPPGLITINGMDRQLVINDLHTHTM 78
QY      89 --GSIHHNGHLQKGTNLHDGANGITCEPPIPPKSGRKRYRKKA-QOYGTSMYHSHEAOY 145
Db      79 VKSTSIHHNGEFGKTTGNWADPAEFINCP--SGSHPELVQYVDQAGTGYHSHLSTOY 137
QY      146 GNGVYAGIQI---NGPASPVPYDTLIG--VPFISQYVYSSADELVETLRKNSGAP---SDN 197
Db      138 CDGLGEPVVYDPPNDPADLVDYDNDTVITLVDMYHVA-----KLGPAEPLGADA 189
QY      198 VLEFNSTAKHPETGECEYANVTLTPGRARRLRILMTSVNHFQVSLVNHITMCIADAVPV 257
Db      190 TLINCKGSPSTTRADLSVISTYETKRRKRFPLVSLSCDPNTFSIDGHNMTIITDSINT 249
QY      258 NAMTVDSLELFGQORYDVIANETPGNYWE--NYTEGGILLGSGSRNPYPALFHYGA 315
Db      250 APLYVYSIQIPAAORISFYLEAGQAVDNYWIRAMPNGWNGVFTGIN---SAILRRDGA .309
QY      316 PGGPPT---DEGKAPVDHNCIDLPLKFPVARDVPLSGFARADNTLDVTLDTTGPFLV 372
Db      306 AAVEPTTQTTSTAP-----LNEVNLHPLVTTAAPGSPVAGVDLAINMAFENGNTFE- 355
QY      373 WKVNSASAINDMGRVAVDYVL-TQNTS--YINLEVENGADQMSYMLIENDCAPF 427
Db      360 --INSTSTPTPVVLLQIISGAONAODLLPSGVYSIAPS-NADIEISFPATAAPGA-- 413
QY      428 TLPHEMHIGHDFYLGSRPDESPASNERHVEFPAERDAG--LISGANPVARDV--SMILPA 483
Db      415 --PHEFHIGHAFAFY-----RKSAGSVYNYNDNIPFDVYSTGPA 455
QY      484 FG-VWVYLSFRADNPGAWLTFCHILAHNHVSGGLGVYVLEFRADLRCAVSDADADDLRLCAD 544
Db      454 AGDNVTIIFERDNDGPMWELHCHIFHELEAGFAVVEADIPDVASA----- 498
QY      543 WRRVYPTNPYKPSDGL 559
Db      499 -----NPVQAWSDL 508

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| ID | LACL CORHI | STANDARD; | PRT; | 520 AA. |
|----|---|-----------|------|---------|
| AC | 002497; | | | |
| DT | 01-OCT-1996 (Rel. 34, Created) | | | |
| DT | 01-OCT-1996 (Rel. 34, Last sequence update) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) | | | |
| DE | Laccase precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase) | | | |
| DE | (Urisinol oxidase) (Urisinolytic phenoloxidase). | | | |
| OS | Coriolus hirsutus. | | | |
| CC | Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; | | | |
| CC | Asphyliophorales; Coriolus. | | | |
| OX | NCBI_TaxID=5327; | | | |
| RM | (1) | | | |
| RP | SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. | | | |
| RC | STRAIN-IFO 4917; | | | |
| RX | MEDLINE=90368706; PubMed=2394718; | | | |
| RA | Kojima Y., Tsukuda Y., Kawai Y., Tsukamoto A., Sugura J., | | | |
| RA | Sakai M., Kita Y.; | | | |
| RT | "Cloning, sequence analysis, and expression of ligninolytic | | | |
| RT | phenoloxidase genes of the white-rot basidiomycete Coriolus | | | |
| RT | hirsutus."; | | | |
| RL | J. Biol. Chem. 265:15224-15230(1990). | | | |
| CC | -1- FUNCTION: MOST PROBABLY PLAYS AN IMPORTANT ROLE IN LIGNIN | | | |
| CC | DEGRADATION. CLEAVES THE C-C AND C-O BONDS OF SOME PHENOLIC LIGNIN | | | |
| CC | MODEL COMPOUNDS (SUCH AS O- AND P-QUINOLS, AMINOPHENOLS AND | | | |
| CC | PHENYLENEDIAMINE). | | | |
| CC | -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2 | | | |
| CC | H(2)O. | | | |
| CC | -1- COPACITOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU | | | |
| CC | CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE | | | |
| CC | 3 OR COUPLED BINUCLEAR. | | | |
| CC | -1- SUBCELLULAR LOCATION: Secreted. | | | |
| CC | -1- POLYMORPHISM: 2 ALLELIC FORMS VARYING IN ONE AA POSITION. | | | |

Best Local Similarity 63.8%; Pred. No. 2e-136;
Matches 356; Conservative 83; Mismatches 113; Indels 6; Gaps 2;

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QY 4 CNTPSRACCTDGVDTVDVENDSPDGVVPTLTLTEDVNTGPGVYKREKMLVNN 63
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 55 CNSPTNQCSPSPFNITDDELGTPTNGTKRRLTLTETDMMTGPGVYKIDKRWVNDN 114
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 64 IIPFTIADMDGTIOVYVNNLETNGTSHHGHGKGTMLHDGANGITECPPIPKGRK 123
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 115 IIPFTIADMDGTIETIVYKIKKNGTSHHGHGKGTMLHDGANGITECPPIPKGRK 174
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 124 VYRFAQOYSTWYSHFSQYQNGVGAIOINGPASYDPLDGLVPISDYYSADDEL 183
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 175 VYRFAQOYSTWYSHFSQYQNGVGAIOINGPASYDPLDGLVPISDYYSADDEL 234
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 184 VELTKNSGAPSDNVLENGAKHPERGESEYANTLTLPGRHRLRLINTSEVNFQVSLV 243
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 235 VILTOHAGPPSPNNVLENGAKHPETTGAGQYATVSLKRGKRLRLINTSEVNFQVSLV 294
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 244 NHTWCITADMDVPMNATVDSLFLGVQORYDVVLEARNFGNWFNTFGGGLCGSSRN 303
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 295 NHTWCITADMDVPMNATVDSLFLGVQORYDVVLEARNFGNWFNTFGGGLCGSSRN 354
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 304 PYPAIFHYAGRGPPDEGKAPVDHNCIDLPLKFPVARDVPLSGFARADNTLDVTL 363
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 355 KYPAIFRYOGAPKALPTNKGVAAPPDHQCIDLNDLKPSLNTNSIALNTGNTIPITL 414
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 364 DTGTPLFVYKNGVSAINIDMGRAVVDVYLTQNTSPFGNIVYVNGADQVSLIENDP 423
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 415 DG----FVWRVNGTAININMKNKPVLEYVMTGNTNYSQSDIVAVEGVNOMKRWLINDP 469
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 424 GAPFTLHPHMLHGHDFYVLRSPDESASNERHVPADAGLLSGANFVRDVMPLA 483
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 470 DGAFSLPHRPHHNDLILGRSPDYALISQTRVFPDPAVDMALNNNTPRRTALMLPA 529
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 484 FGVVYLSFRADNCGAMLFCHIHAMHVSGLGVYLERADLRGAVSDADDLRLCADW 543
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 530 KGMILLIFRDRNPGSWMLHCHIAMHVSGLSNOLFLERADLRNLSISPAKKAFFNDNDAM 589
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 544 RRYWPTN-PYKPSDSGLK 560
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 590 RAYFPDNPAPPKDDSGLR 607
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: M73257; AAA33105.1; -.
DR EMBL: S38903; AAA09235.1; -.
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicopper oxidase2.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
KW Glycoprotein; Repeat.
FT SIGNAL 1
FT CHAIN 21
FT DOMAIN 66
FT DOMAIN 198
FT DOMAIN 416
FT METAL 126
FT METAL 128
FT METAL 171
FT METAL 173
FT METAL 463
FT METAL 466
FT METAL 468
FT METAL 533
FT METAL 534
FT METAL 535
FT METAL 539
FT METAL 539
FT CARBOHYD 121
FT CARBOHYD 121
FT CARBOHYD 234
FT CARBOHYD 242
FT CARBOHYD 265
FT CARBOHYD 323
FT CARBOHYD 407
FT CARBOHYD 425
FT CARBOHYD 425
SQ SEQUENCE 591 AA; 64696 MW; B2F44CB2AD77701 CRC64;

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Query Match 58.5%; Score 1849; DB 1; Length 591;
Best Local Similarity 59.9%; Pred. No. 3.3e-124;
Matches 337; Conservative 74; Mismatches 144; Indels 8; Gaps 6;
QY 1 QOSCNTPSRACCTDGVDTVDVENDSPDGVVPTLTLTEDVNTGPGVYKREKMLV 59
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 33 QPNCNTASNRACCTDGVDTVDVENDSPDGVVPTLTLTEDVNTGPGVYKREKMLV 92
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 60 VNNISIGPTTFADMDGTIOVYVNNLETNGTSHHGHGKGTMLHDGANGITECPPIPK 119
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 93 VNGNIIILPVIHAQMGDTISTVYNNLKYNGTTHHGHGKGTMLHDGANGITECPPIPK 152
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 120 GGRVYLFYKKAQOYSTWYSHFSQYQNGVGAIOINGPASYDPLDGLVPISDYYS 179
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 153 GGSYTYFIHAYOYSTWYSHFSQYQNGVGAIOINGPASYDPLDGLVPISDYYS 212
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 180 ADELVELTKNSGAPSDNVLENGAKHP-ENGEGSEYANTLTLPGRHRLRLINTSEVNF 238
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 213 ADELVELTKNSGAPSDNVLENGAKHP-ENGEGSEYANTLTLPGRHRLRLINTSEVNF 272
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 239 QVSLVNTKCIADMDVPMNATVDSLFLGVQORYDVVLEARNFGNWFNTFGGGLCG 298
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 273 QVSLVNTKCIADMDVPMNATVDSLFLGVQORYDVVLEARNFGNWFNTFGGGLCG 332
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 299 GGSNRPYPAIFHYAGRGPPDEGKAPVDHNCIDLPLKFPVARDVPLSGFARADNT 358
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```


RESULT 14

S18746

laccase (EC 1.10.3.2) - basidiomycete (Phlebia radiata)

C:Species: Phlebia radiata

C:Date: 22-Nov-1993 #sequence, revision 10-Nov-1995 #text, change 11-Jun-1999

C:Accession: S18746

R:Salomonio, M.; Niku-Paavola, M.L.; Knowles, J.K.C.

J. Gen. Microbiol. 137, 1537-1544, 1991

A:Title: Isolation and structural analysis of the laccase gene from the lignin-degrading

A:Reference number: S18746; MUID:92055223; PMID:1955850

A:Accession: S18746

A:Molecule type: DNA

A:Residues: 1-548 <SAL>

A:Cross-references: EMBL:X52134; MID:g3257; PIDN:CAA36379.1; PID:g3258

C:Genetics:

A:Initons: 61/3; 84/3; 125/1; 163/1; 184/2; 217/2; 269/3; 336/3; 355/3

C:Superfamily: laccase

C:Keywords: oxidoreductase

Query Match

Best Local Similarity

Matches 162; Conservative 66; Mismatches 195; Indels 90; Gaps 22;

17.6%; Score 556; DB 2; Length 548;

Pred. No. 6e-33;

Query 49 PDGVYKRWLVNNSITGPTIFADMGDTIOVTYVNNLETNG-----TSIHMGHLQKGTN 103

Db 38 PDGSRQAV-LAEGVFPGLIAGNKGDNFQINVIDEL-TNATMLKTTTIHMGHFGHGTN 95

Query 104 LHDGANGTECPPIPKGGRKRYRKA-QQVGTSMYSHFSQYGVGATQINGPASP 162

Db 96 WADSPATINQCFI-ASGDSFLYNFQVDPQACTFWYHSLSTQYCDLGRPVVYDPA-D 153

Query 163 Y-----DTDLGVPPISDYYSADDELVELTKNSGAPF--SDNYLFNGTAKHPETG--EG 212

Db 154 YLDQYDDDDSTVITLADWYHTAA-----RLGSPRPADDTLNLINGLRCGEGAGCVS 205

Query 213 EXAVNTLTPGRHRLINTSVENHFOVSLVNHMCITADNVNANTVDSLGVGQR 272

Db 206 DLAVISYVTKGRYRFLVSIQDSFFTSIDGHSIMLEVATNHPDLTVDELITVAGOR 265

Query 273 YDVVIEANRTPGNVFWNTFFGGILCG--GSRNPYPALIFHYAGAP--GGPPTDEGKAPVD 329

Db 266 YSFLITLADQDQDYNWIRANPGIITGTGAGIN---SAILKTDGADVETPTTQATSYV- 321

Query 330 HNCIDLPLKRVAVADVPVLSGFARADNTLDVTITDTGTPLEFWKVGSAIINIDGRAV 389

Db 322 --VLSSENLAPLTNAAPGLPEVGVLDLALNFNLTFDG-PALKFQINGV----- 367

Query 390 DYVLTQNTSPPGYNIV--EVNGADQMS-----YWLIND-----PGAPFTLPHRM 433

Db 368 -----TFVPPYVPLLIQIISGAOSADLLPSGSVYALPSNATTELSPFAGALGGPHF 420

Query 434 HLHGHDEYVLGRSPDESASNERHVPFAPDAGILSGANPFRDVSMLPAG--WVLSFR 492

Db 421 HLHGHFSV-----RRAGSTYNY-----VNPQRDVYSIGNGDMVTIRFD 463

Query 493 ADNPGANLFRCHITAMHYSGIGVYTLERADDLR 525

Db 464 TNNGPWFHLCHIDMHLAALPLSLRTSLTLR 496

RESULT 15

T05020

L-ascorbate oxidase (EC 1.10.3.3) - Arabidopsis thaliana

N:Alternate names: protein T19P19.220

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 23-Apr-1999 #sequence, revision 23-Apr-1999 #text, change 16-Jul-1999

C:Accession: T05020

R:Bevan, M.; Monfort, A.; Casacuberta, E.; Puidomenech, P.; Hohensei, J.; Mewes, H.W.;

submitted to the Protein Sequence Database, April 1998

A:Reference number: Z15394

A:Accession: T05020

A:Molecule type: DNA

A:Residues: 1-582 <BRV>

A:Cross-references: EMBL:AL022605

A:Experimental source: cultivar Columbia; BAC clone T19P19

C:Genetics:

A:Map position: 4

A:Initons: 98/3; 129/3; 200/3; 265/3

A:Note: T19P19.220

C:Superfamily: laccase

C:Keywords: oxidoreductase

F:381-577/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>

F:51-234/Disulfide bonds: #status predicted

F:92/486/Binding site: copper (His) (type 2) #status predicted

F:94/136/138/488/545/547/Binding site: 2Cu-O cluster (His) (copper type 3) #status f

F:113-577/Disulfide bonds: #status predicted

F:195/398/481/551/Binding site: substrate (Trp, Trp, Glu, His) #status predicted

Query Match

Best Local Similarity

Matches 157; Conservative 91; Mismatches 215; Indels 143; Gaps 21;

17.3%; Score 547.5; DB 2; Length 582;

Pred. No. 2.e-32;

Query 4 CNTPSNRACWTDGYDINDYEDSPDTGVVRYPTLTLEVDNMTGPDGVYKRYLVNNS 63

Db 31 CQGIKRRFKW-----EYKIEFKSPD-----CEKLVITTINGK 62

Query 64 IIGPTIFADMGDTIOVTYVNNLETNGTSIHMGHLQKGTNLDGANGTECPPIPKGRK 123

Db 63 FPGPTIKAOQGDITVELKNSFMTENVAHVHGIROIGTPEDEGVGTCPIIP-GEVF 121

Query 124 VYRKAQOYGTSMYSHFSQYGVGATQINGPASP-----YDVLGVPPISDYYS 179

Db 122 IYQFVVRPRTGYMHSYHGQRESGLIGMTQVSPATEPEFTYDYDRN-FLTLDMYHKS 180

Query 180 ADELVELTKNSGAPFS-----DNVLFNGTAKH-----PETGEGERANY----- 217

Db 181 MSE--KATGLASIPFKWVGEPQSLMIGRGFRNCSNLTTPSLYSGCVSNADCSRFI 238

Query 218 -TLTPGRHRLRLINTSVENHFOVSLVNHMCITADNVNANTVDSLGVGQRYDV 276

Db 239 LTVIPGKTYRLRLISLALSLSFQIGHNLTVEADGHVEPPTVKNLEFVSGEFTSVL 298

Query 277 IEANRTP-GNVWFVWTEGGGLCGSRNPYPALIFHYAGAP--GGPPTDEGAPVDHNCID 334

Db 299 LKADNPRRNTWITSSI---VSRPATTPTATVAVNTYTPNHPRRRRPTSESS----- 346

Query 335 LPNLKP-----VVARVPLSGFAKRAADNTLDVTITDTGTPTLFWKVG-- 377

Db 347 --NIVPEMNDPRLSLAQSIAIKARGFTHALPENSDEVIL-VLNTQN-----EVNGYRR 397

Query 378 -SAINIDGRAVDYV--LQNTSFPFGYINVEYNGADQMSYMLI----- 419

Db 398 WSVNNSVYHHPKPTYLALQNLNAPDMRTAPENDYSRNYDIFAPPLANATTSQGIY 457

Query 420 -----ENDPGAPFTLPHPMHLHGDFYVIGRSPDESASNERHVPDAPDA 465

Db 458 RLRRNSTVDVLIQANATNMANNSTHFMHLHGDFVWLGIGEGK-----FNESBDP 508

Query 466 GLLSGANPVRDVSMLPAGFVYVLSFRADNPGANLFRCHITAMHYSGIGVY---LERAD 522

Db 509 KRYNRVDPPIKKNVAVOVPFGWLTALFRADNPGVMSFCHIESHFQMGYIFESGIDKYS 568

Query 523 DLRCAY 528

Db 569 SLPSI 574

Search completed: December 4, 2002, 10:46:54
Job time: 24 secs

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QY 307 AALFYAGPGPPDEKAPV-----DHNCIDLPKPVYARVPLSGAKRADNTLDT 362
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 301 SAILRYDAEDIEPTNATSVPLETDLVPLDN---PAAPGDPQVG---VDLMSLD 354
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 363 LDYTPLEFV-----WKVNGSAINIMGRAVYVLTONT 397
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 355 EEFNSNFNNETVPPVPLVLQILSGAQAASLLPMSV-----YTLPSNS 403
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 398 SEPPGYIVEVGADQMSYMLIENDPGAPFTLPHPMHLGHDFYLGSPDESASNERH 457
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 404 TLEISFPIITDG-----VLNAPGA---PHFHLGHFESVY-----437
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 458 VEDPARDAG--LLSGANPYRD--VSMLEPAFGWVLSFRADNGAMLFCHIANHVGGLG 514
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 438 -----RSAGSSTFNANPYRBDTVSGNSGDNVITFTTDMNPGMFLHCHIDPLEAGFA 492
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 515 VYLERADDLRGAVSDADDDLRLCADRRYPTNPKYKSD 557
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 493 IWMGE-----DTADTASANPYPTAMSDLCP--YDALDS 524
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 10

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JCS355
laccase (EC 1.10.3.2) 3 precursor - white-rot fungus (Trametes villosa)
N:Alternate names: Urushiol oxidase
C:Species: Trametes villosa (white-rot basidiomycete)
C:Date: 28-May-1997 #sequence_revision 28-May-1997 #text_change 19-May-2000
C:Accession: JCS355
R:Laver, D.S.; Golligly, E.J.
Gene 181, 95-102, 1996
A:Title: Cloning and characterization of three laccase genes from the white-rot basidiom
A:Reference number: JCS355; M01D:97128774; PMID:8973514
A:Accession: JCS355
A:Molecule type: DNA
A:Residues: 1-512 <YAV>
A:Cross-references: GB:L78076
C:Comment: This enzyme is a multi-copper enzyme which catalyzes the oxidation of phenol
pathogenesis.
C:Genetics:
A:Gene: lacc3
A:Introns: 61/3; 84/3; 125/1; 163/1; 184/2; 211/2; 263/3; 330/3; 349/3; 416/3; 455/3; 49
C:Superfamily: laccase
C:Keywords: oxidoreductase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:12-512/Product: laccase 3 #status predicted <MAT>

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Query Match 18.1%; Score 573; DB 2; Length 512;
Best Local Similarity 30.5%; Pred. No. 3,1e-34;
Matches 164; Conservative 72; Mismatches 214; Indels 88; Gaps 18;

QY 40 LTVVD---NMTGPDGVYKERMVNNSTIGPTIADMGDTIQVYINNLET---NGTSI 92
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 26 VTELIVNVKVIAPDGAARDTV--LAGTFPGPLITGKKGKGNFRINVDKLVNQMLSTTI 84
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 93 HHNGHLOKGTNLHDGANGTECPPIPKGGRKRYRKA--QOYGSWHSHESSAQYGVG 131
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 85 HHNGHLOKGTNLHDGANGTECPPIPKGGRKRYRKA--QOYGSWHSHESSAQYGVG 131
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 152 AIOI---NGPASILPYDTD--LGVFPISDYSSADELVELTKNSGAPFSDNVYFNGTAKH 206
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 144 PLVITDHPDPAQVLYDVDEDSYITLADMYHPPAPLLPPAA-----TLINGLGRW 193
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 207 PETGESEYANVLTIGRRRLRLINTSVENHFOVSLVNHITMCIADMPVNMATYDSLF 266
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 194 PCNPADLAVIEVQHKRRFRFLVSTSCDPNMYFTIDGHTMTIIEADGONTOPHOVDGLQ 253
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 267 LCVGORYDVVIEANRTPGVYWF-----NVTPGGGLGGSNSNPYPALEFHYAGAPGP 319
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 254 IIRAQRTSYVLANNAQVANNITWIRANRANNT-----GPAANGINSALIRKKGAPLKE 305
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 320 PDEGKAPVDHNCIDLPKPKPVYARVPLSGAKRADNTLDTLTGTPLFYWKVNGSA 379
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 306 PTT--NQTIRNFMETDLHPLTDPRAPGLPFKGVDAHALNMLTFNGSEFFINDAPFV 363
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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QY 380 INIDGRAVDVYLTONTSEPPG--YNI-----VEVNGADQMSYMLIENDPGAPFTLPHR 432
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 364 PTVVLLQLINGTLANDLILPGSYNNLPPDSTIEL-----SIPGVTGPGPH 411
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 433 MHLAGHDFYLGKSPDESASNERHYFDPARDAGLLSGANPYRARD--VSMLEPAFGWVLSF 491
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 412 FHLHGAFTSV-----RSAGSTEYNY-----ANPYRBDTVSGISGLADNVTYR 454
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 492 RADNPGAMLFCHIANHVGGLGVYLERADDLRGAVSDADDDLRLCADRRYPT 549
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 455 VTDNPGMFLHCHIDPHLDAGLAIVFAEDAQDTK-----LVNVPEDMNKLCP 503
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 11

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A36962
laccase (EC 1.10.3.2) precursor - fungus (Filobasidium floriforme) (ATCC 34873)
N:Alternate names: diphenol oxidase
C:Species: Filobasidium neoformans, Cryptococcus neoformans
C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 13-Mar-1998
C:Accession: A36962
R:Williams, P.R.
J. Bacteriol. 176, 656-664, 1994
A:Title: Biochemical and molecular characterization of the diphenol oxidase of Crypt
A:Reference number: A36962; M01D:94131944; PMID:8300520
A:Accession: A36962
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-624 <WII>
A:Cross-references: GB:L22866
C:Genetics:
A:Gene: CNLAC1
A:Introns: 25/3; 69/3; 117/1; 137/3; 176/2; 204/2; 223/3; 238/3; 371/2; 391/2; 426/3
C:Superfamily: laccase
C:Keywords: copper; glycoprotein; oxidoreductase

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Query Match 18.0%; Score 568; DB 2; Length 624;
Best Local Similarity 29.9%; Pred. No. 9,5e-34;
Matches 174; Conservative 86; Mismatches 218; Indels 104; Gaps 29;

QY 17 YDINTYEV--DSPDGVVRPYTLTLEVDNMTGPDGVYKERMVNNSTIGPTIFADMGD 75
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 47 FALSNDPEITDVFPT---RETFDIAKA--FASPDGIERE--YVVMNMPGPVTEANTSD 100
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 76 TIOVYINNLETNGTSIHMHGLOKGTNLHDGANGTECPPIPKGGRKRYRKA--AOOYGT 134
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 101 TIVVHNNHLD--EGSLHHHGLRLQLTGAFMDGVPTGCTIPF--GGSFYTNFVSHQGT 158
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 135 SWHSHFSQAQYGVGAQIQNP-----ASLPYTDLGVFPISDYSSADELVELTK- 188
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 159 YMMHSHYSNSMADGIMGPLIVHSPNEPLRGDRDYEDRIVE--ITDMHNDSELIITAAAL 217
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 189 -----NSGAPFSDNVYFNGTAKHNPETGEYEA-----NVTLTGRRHRLINTSYE 235
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 218 PEYTKGNIAAPQGDAILINGRGQNTANTAGSSCFPRPEIIOVPANCYKRLRFISATIH 277
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 236 NHPQVSLVNHITMCIADMPVNMATVDSLFLVGORYDVVIEAN--KPPGNTWFWTEG 293
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 278 PMYRISIDNPMVEVADGAAYVGPVTHEISVAPGERYSALINTNGKKEGDAFWLRTSV- 336
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 294 GGLIC--GGSNPNPRAIMFYAGAPGPPTDEGAAPYDHNCLDLPKPVYARVPLSGFA 352
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 337 -ALSCMGAVSOEGGLAVVRRTG--NGAVSTEE--PQTSAMSDIAGV-----TPCTGL- 384
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 353 KRADNTLDV---TLDTTGTPL---FVWKVNGSAINI-----DMGRAVDVYLTONTSE 399
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 385 ---DQYTLSPRSLAPAREPLQSHFNSBERGAFVAVLGATPGCYGFNNISY---QNOQF 438
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 400 PEGYNIVEVNGADQMSYMLIENDPGAPFTLP-----HPMHLGHDFTV 442
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 439 NPLISTIVQKGS-----CENTLVSSRTFPPDGPNGNIIINLDVYIDHPYHLHGNEFOV 491
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 443 LGRSPDESASNERHYFDPARDAGLLSGANPYRARDVSMLEPAFGWVLSFRADNPGAMLFH 502
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 144 PFVVYDNDPHASLYDVNDNDFVITTLADWHTAA-----KLGPAPFLGADATLNGL 195
 QY AKHPEGESEYANTLTFRHRRLRLINTSEVNHFOYSLVNTMCTIAADWPNAMTYD 263
 Db 196 GRSSSTTAADLAIVNTKGRKRRRLVSLSCDPNHTSISDHDTLIEVDSINQPLVVD 255
 QY 264 SLFLVGORVDVIEANRTPGNYWF--NWTEGGILCGSRNPYPALIFHAGAPGPP 321
 Db 256 SIQFAORSEFVLNADODVGNWIRANPNNGVAPAGIN-----SALIRIDGADPEPT 311
 QY 322 DEGAAPVDHNCIDLPNKPVYARVPLSGFRKRDNTLDVLTDTGPLEYWKVNGSAT- 380
 Db 312 TGTQTPP--KPLANEVDLHPPLATMAVPGSPVAGVDTAINMAFNNGTFF--TNGASFV 366
 QY 381 --NIDMGRAVVDVYL/TONTSEPPG--YNIYEVNGADQMSWVLENDGAPFLPRLPHLH 436
 Db 367 PPIYVYLQITISGQNMADLLPGSVYSLPS--NADIELSPATAAFGA----PHEPLH 421
 QY 437 GHDFYVLGRSPDES PASNERHVPDPADAG--LLSGANPYRVDY--SMLPAFG--WVYLSF 491
 Db 422 GHAFAYV-----RSAGSTVYNDNPIPROVYSTGPAPAGDNTIRF 462
 QY 492 RADPGAMLFCHITAMHVSGLGVYLERADDLRGAVSDADADLDRLCADMKRYPTNP 551
 Db 463 RTDNPGEWFLCHIDFHEAGFAVFAEDIPDVASA-----NP 500
 QY 552 YPKSDSGL 559
 Db 501 VPQWMSDL 508

RESULT 6

S68120
 Laccase (EC 1.10.3.2) 4 precursor - Rhizoctonia solani
 C:Species: Rhizoctonia solani
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
 C:Accession: S68120; S77976; S72364
 R:Wahlthner, J.A.; Xu, F.; Brown, K.M.; Brown, S.H.; Gollightly, E.J.; Halkier, T.; Kai
 Curr. Genet. 29, 395-403, 1996
 A:Title: The identification and characterization of four laccases from the plant pathoge
 A:Reference number: S68117; MUID:96171523; PMID:8598061
 A:Accession: S68120
 A:Molecule type: DNA
 A:Residues: 1-529 <MAN1>
 A:Accession: S77976
 A:Molecule type: protein
 A:Residues: 20-53;132-180;203-217;378-396;440-465;489-513;520-529 <MAN2>
 R:Wahlthner, J.A.
 submitted to the EMBL Data Library, September 1995
 A:Reference number: S72364
 A:Accession: S72364
 A:Molecule type: DNA
 A:Residues: 1-417, 'CAQHHR', 424-469, 'A', 471-483, 'CT', 484, 'R', 486, 'GSH', 490, 'S', 492, 'PRP',
 A:Cross-references: EMBL:Z54277; NID:g1150567; PIDN:CA91042.1; PID:g1150568
 C:Genetics:
 A:Gene: lcc4
 A:Introns: 56/3; 70/3; 82/3; 87/3; 101/1; 126/2; 143/1; 147/1; 170/2; 193/2; 250/3; 276/
 C:Superfamily: laccase
 C:Keywords: copper; oxidoreductase
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-529/Product: laccase 4 #status experimental <MAT>

Query Match 19.4%; Score 612.5; DB 2; Length 529;
 Best Local Similarity 30.6%; Pred. No. 4; le-37;
 Matches 175; Conservative 73; Mismatches 202; Indels 121; Gaps 24;

QY 25 VDSGCVVAPRYLTLEVENMTGSPGVKEKVLVNNSTIGPIFDMDGTQVYINN 84
 Db 14 VSPFAFAVNNYKFDINNV--VAPDS--FQPIYVNGVLPGTLTANKDPTLRINVT 70
 QY 85 LE---TNGTSIHMHGKHOKGTNLHDGANGITECPPIPKGGRKYRKAQ---QYGSWY 137
 Db 71 LTDPMSMRATTIHHGFLQATTADEDEGPATVTCPI---AQNLSYTEIRPLHOGTGIMWY 127

QY 138 HSHESAQYNGVGAIOI---NGPASLDPYDND--LSGFPISDYXXSSADELVE---LTKN 189
 Db 128 HAHLASQYVGLKRPDLTYDNDPHKSRDYDDASTVWMLMEDWYHTPAPVLEKQMFSTNN 187
 QY 190 SG--APFSDVNLFGTAKHPEGESEYANTLTFR-----GRRHRLRLINTSEVNHFO 239
 Db 188 TALLSPYDGLIN-----GKGRVYGGPVRVRSYINIKRGRRLRYINASATISFT 239
 QY 240 VSLVNTMCTIAADWPNAMTYDSLFLVGQRYDVIEANRTPGNTWFN--VTEGGGL 297
 Db 240 FSIEGRLVTEADGIEHOPLPVDSFOIYAGQRSYVIEANQFANWIRAPMTVAG--- 296
 QY 298 CGGSRNPRPA--AIFHAGAPGPPDE-----GKAPVDHNCIDLN----- 337
 Db 297 AGTIANADPTNVRVAVLHEGAPNAEPTTEGSAIGTALVEENHALINPGAPGSSADAV 356
 QY 338 -LKPVVAROVPLSGFARADNTLDVLTDTGTPLEFWKVGSAINIMGRAVVDVYLTON 396
 Db 357 SIMLAIGRST--VDGILAFTEFNNIKYEAPSLPTLLKILANAS-----NDADFTNEH 407
 QY 397 TSFPPGNIYEVN---GADQMSWVLENDGAPFLPRLPHLGHDFYV--LGRSPDES 450
 Db 408 TIVLPNKKVIELNITGAD-----HPILHGHVFDIVKSLIGTPTNY- 448
 QY 451 PASNERHVPDPADAGLLSGANPYRVDYSLPARGVYLSFRADNPGAMLFCHIAMHVS 510
 Db 449 -----VNPPRDVYRVGGTG--VLAERKTDNPGPMVYCHIDWHLE 487
 QY 511 GGLGVYLERADDLRGAVSDADADDL--DRLC 540
 Db 488 AGALVAEAPASQIRQGVQSVQPMNMANQIC 518

RESULT 7

JC5356
 Laccase (EC 1.10.3.2) 4 precursor - white-rot fungus (Trametes villosa)
 N:Alternate names: urushiol oxidase
 C:Species: Trametes villosa (white-rot basidiomycete)
 C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
 C:Accession: JC5356
 R:Yaver, D.S.; Gollightly, E.J.
 Gene 181, 95-102, 1996
 A:Title: Cloning and characterization of three laccase genes from the white-rot bas
 A:Reference number: JC5355; MUID:97128774; PMID:8973314
 A:Accession: JC5356
 A:Molecule type: DNA
 A:Residues: 1-520 <YAV>
 A:Cross-references: GB:U78077; NID:g1322078; PIDN:AB47734.1; PID:g1322079
 C:Comment: This enzyme is a multi-copper enzyme which catalyzes the oxidation of phe
 C:Genetics:
 A:Gene: lcc4
 A:Introns: 62/3; 85/3; 126/1; 185/2; 217/2; 269/3; 335/3; 424/3; 463/3; 503/1
 C:Superfamily: laccase
 C:Keywords: oxidoreductase
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-520/Product: laccase 4 #status predicted <MAT>

Query Match 19.1%; Score 603; DB 2; Length 520;
 Best Local Similarity 32.2%; Pred. No. 2e-36;
 Matches 180; Conservative 76; Mismatches 211; Indels 92; Gaps 24;

QY 30 TGVVAPRYLTLEVENMTGSPGVKEKVLVNNSTIGPIFDMDGTQVYINN--E 86
 Db 21 SAIGVYTDLTISNGD--VSPDSFTRAAY--LANGVPPGLITGKNGPQINVIDNLSNE 77
 QY 87 T--NGTSIHMHGKHOKGTNLHDGANGITECPPIPKGGRKYRKAQ---QYGSWYHSHFSA 143
 Db 78 TMLKSTSIHHGFFQKGTNADGAFAVNCPI--ATGNSFLYDPTADQAGTFYHSHLSFT 136
 QY 144 QYNGVYVGAQIUNGPSLPI-----DTDLGVPIPSIDYIYSSADELVELTKNSGAPF--- 194

| | | | |
|----|-----|---|-----|
| Db | 226 | DVLEVEFTWNGGPRPSPDYLFVFGHGKKNQGTAGKRAVNTLFRGKHKRLRIITINTSHDHFOJ | 285 |
| Qy | 241 | SLVNHITKCIADADVPVNAAMTVDSLEFLGCGORDVITEANKTPGNTFNFVTFGGGLCGG | 300 |
| Db | 286 | KLOMNTMTIITADADVPVOAQVDSLEFLVAGGRDYVTIDANKSVGNWFNFTEFGGLACGA | 345 |
| Qy | 301 | SRNPAPAIFFYACAGPGGPDEDEKAPVDHNCIDLPMILKVVYARDVLSFAKARANDTID | 360 |
| Db | 346 | SLNHPRPAVFRYQCAPNTLPNTINITPRADANCMDLNLTPVSSVSTSGPTSPRPNNTLP | 405 |
| Qy | 361 | VTLDITGTPLEFVMKVNCSAINIDMGRAVVDVYLQNTSPFPYGNIVEVNGADOMSWYLE | 420 |
| Db | 406 | VSLTGTGTPLEFVMKVNCSAINVMDKPIVDYVLIQNTSTPPQANVLTVNSVQNTWTWLE | 465 |
| Qy | 421 | NDDCAPFTLPHRPHMLHGDFVYLCRSPDESA--NRRHVTDPARADGLSGANPPVRDY | 478 |
| Db | 466 | NDDPSPESIPHRPHMLHGDFLTVRSPDQ--PAGVPQTRYFPNRPATDALLKSSNPVRDY | 524 |
| Qy | 479 | SMLPAGFVNVSPFRADNGALFLFCHITAMHNSGGLGAVVYERADDDGAVSDADADDLR | 538 |
| Db | 525 | AMLPANGMLLIAFSSDNGALFLFCHITAMHNSGGLSVQYLERPDDLRFNGFSQADKQNHNN | 584 |
| Qy | 539 | LCADMRRTVPNPYPKSDSGIK--HRWY--EBGSEWLVK | 572 |
| Db | 585 | NCNAMRAVWPNPEPKIDSGILTKVKKVWGEHNDWYIK | 620 |

RESULT 2

4 CMTSPNACMGWDGVDIMNDYEDSDPTGCVRRYYTLTLEVDNMTTPDGGVYKAKLVNNS 63
||||||| ||| :||:||||||| :||| | ||||| ||| |||||:|||||||:

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Db 55 CNSPTNRQNCBPGFNINTDVELGPTPNCKTRRYTLTLETDNMIGRPGVAKKDYMAVYNDK 114
OY 64 IIGPTIFADMGDTTOVTVINNLLETNGTSHHGHGKOTMLHDGANGITECPIPRKGGRK 123
Db 115 IIGPTIQADMGDTTEIFYINKLNGTSHHGHGKOTMLHDGANGITECPIPRKGGSK 174
OY 124 VYRFEAAOQYGTSMWHSHESAOYGNGVYGALDINGPASPITDTCVFPISDIYSSADEL 183
Db 175 VYRWRATQYGTSMWHSHESAOYGNGVIGPRTYVINGPASANDVLDGEPPLDIYYDPADEL 234
OY 184 VELTNSGAPSDNVLFNGTAKKHETGEGETANYTLPGRRHRLRLINTSEVNHPOVSLV 243
Db 235 VLLTDHAGPPSSNNVLENGFAKHPTTGAGQATVSLTKGKHRLRLINTSEVNHPODLLV 294
OY 244 NHTMCLIAADWVPVAMVNVSLPEFGVQORYDYVEANRTGANTWFNTYTFGGGLGCGSRN 303
Db 295 NHSMTIISADLVPOQYKVDSLFLGVOQRDVIIDANQVANGVTFWNTFBGSGSLCDSDN 354
OY 304 PYPAIFHYAGAPGPPDESGAFVVDHNCIDLPLNKRFVAVADVPLSGEAFKADNTLDVTL 363
Db 355 HYPAIFRYQCAPALPFTNCGAVAVDHCQDLNDLTKPVLQRSINTNSIALNTGNITPIL 414
OY 364 DTGPTPLFVKKVNCSATINIDMGRAVVDVYLTQNTSPFPGNIYIEVNGADOMSTMLENDR 423
Db 415 DG-----FVMYVNSTAININMKRYLVEYLTGNTNSQSDNIYQVEBVNMOKTWMLLENDP 469
OY 424 GAPTLPHPMHLHGDFEVLGRSPDESPASNERIVTFPPADAGLLSGANVVRDYVMPLA 483
Db 470 DGABSLPHRPHLHGDFLILGRSPDYVAISOTRYVPPADAMARLNGNNTFRDQTMPLA 529
OY 484 FGWVVLASFRAFGAMLFFCHIAHNVSGLGVLVYTLERADDLRCGAVSDADADDLRLCADM 543
Db 530 KGMILLIARTDNPSCSMILMHCHIAHNVSGLSNGLEBAQDLRNSISPADKKAFAVNDGAM 589
OY 544 RRYMPTN-PRYKSDSGLK 560
Db 590 RAYFPDNPAPFKDDSGLK 607

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RESULT 3

KSNCLT
 Iaccase (EC 1.10.3.2) precursor - Neurospora crassa (strain TS)
 M:Alternate names: urishiol oxidase
 C:Species: Neurospora crassa
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
 C:Accession: B28523
 J:German, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
 J: Biol. Chem. 263, 885-896, 1988
 A:Title: Characterization of two allelic forms of Neurospora crassa Iaccase. Amino-
 A:Reference number: A28523; MID:88087214; PMID:2961749
 A:Accession: B28523
 A:Molecule type: DNA
 A:Residues: 1-619 <GER>
 A:Cross-references: EMBL:M18334; NID:g168827; PIDD:AAA33592.1; PID:g168828
 C:Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquinol
 C:Genetics:
 A:Introns: 86/3
 C:Superfamily: Iaccase
 C:Keywords: copper; glycoprotein; oxidoreductase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-49/Domain: propeptide #status predicted <PRO>
 F:50-619/Product: Iaccase #status predicted <MPT>
 F:84-215/Domain: amino-terminal beta-barrel #status predicted <BB1>
 F:216-372/Domain: middle beta-barrel #status predicted <BB2>
 F:431-580/Domain: C-terminal beta-barrel #status predicted <BB3>
 F:133,282,295,340,422,444/Binding site: carboxylate (Asp) (covalent) #status predicted
 F:144,480/Binding site: copper (His) (type 2) #status predicted
 F:146,189,191,482,548,550/Binding site: 2Cu-O cluster (His) (copper type 3) #status
 F:477,549,554/Binding site: copper (His, Cys, His) (type 1) #status predicted
 Query Match 64.0%; Score 2021; DB 1; Length 619;
 Best Local Similarity 63.8%; Pred. No. 2,2e-140;
 Matches 356; Conservative 83; Mismatches 113; Indels 6; Gaps 2;

Wed Dec 4 15:07:58 2002

us-09-869-877-10.rapb

Page 10

[illegible]

Search completed: December 4, 2002, 10:51:23
Job time : 14 secs

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QY 171 PISDYVSSADELV--ELTKNSG-APESDNYLFNGTA--KHETGEGETYANVTLPGRH 225
D 163 IILGEMKSDIRAVONEFLGNGDANVSDAFLINGOPDILPCSRSDTY-MLTYESGKTY 221
QY 226 RLRLINTSVENHFPVSLVNHMTCLADNVVNMATVDSLFLVGQRIDVYIEANRTPGN 285
D 222 LIRMINAVMTIMEFSIANHSVTVGSDAATKPLKSDYITISPGOTIDFLAQNTPSH 281
QY 286 YMFVNTGGGLLCGSRNPYPALFHYAG--APGPR----- 319
D 282 YV--MAARAVALVAGNPNMTTITAIIRKGNATASPSFPLMGPENDTNASVNTYILKRS 339
QY 320 -----PTDEGKAPVDH-----NCIDLPN-----LKPVVA--- 343
D 340 LGNKNYEVDPVKNTDKLLFPFSINLPPCPNNSCAGPENEPFRASVNNITFPPTIALQ 399
QY 344 -----RDVPLSGPAKADNTLDVTLDTGTPPLVWK-VNGSAINIDGRAVVDVYLTON 396
D 400 AYYORINNYVSNPNPSPFPFNTYSDI--IPRDLMPQONTEVKYKLNSTVEIVE-OG 456
QY 397 TSFPPGYNIVEVNGADQMSYMLIENDPGAPFTLPHPHLGHDPYVLGRSPDESASMER 456
D 457 TNLAG-----IDPHLHGOSFTYVWG-----LGNFN 485
QY 457 HVEDPADAGLISGANPYRDVSMPLPAFGVYLSFRADNPGAMLFCHIAMHVSGLGV 516
D 486 NATDPLN-----YNLVDPLMNTIAVPVSGWAVAFKASNPQVWLHCHLERNHLSMGDMV 541
QY 517 YL 518
D 542 FI 543

```

RESULT 12

```

US-09-942-185-2
; Sequence 2, Application US/09942185
; Patent No. US20020165113A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Convents, Daniel
; APPLICANT: Doornink, Monique
; APPLICANT: van Gastel, Frans
; APPLICANT: Rodrigues, Ana
; APPLICANT: Topozada, Amr
; APPLICANT: De Vries, Cornelis Hendrikus
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: Detergent Compositions Comprising No. US20020165113A1el Phenol OX
; FILE REFERENCE: C7567
; CURRENT APPLICATION NUMBER: US/09/942,185
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Stachybotrys Chartarum
US-09-942-185-2

```

```

Query Match 7.6%; Score 241; DB 9; Length 583;
Best Local Similarity 25.0%; Pred. No. 9.8e-13;
Matches 152; Conservative 59; Mismatches 226; Indels 170; Gaps 32;

```

```

D 169 ARMLYHDHANSITAENAYMGAGYMIODPAEDALMLPSGGEDEI-----PLVL 219
QY 186 LTKNSGAFSDNYLFNGTAKHPERGE-----GEYANTLTP-----GRHRRLINTS 233
D 220 TAKRYNA-----DGLTFS-----TNGEVSSEWGDVYOVNGOPMILNOPRKTRRFLNAA 270
QY 234 VENHFQVSLVNH-----TWCIIAAD-----MVVNAMATVDSLFLVGQRIDVYIEANRT 282
D 271 VSRFSALYIATSEDESETRLPQVYIAADGGLLEGVD--PTLVIISMERREVIDS-- 325
QY 283 PGNTFVNTFEGGLLCGSRNPYPALFHYAGA-----PGPPTDEGKAPVDHNCIDL 336
D 326 -----TEAGOSI-----DIRMLPGAAGLIGVEPEFDWTDKVMRFVDEVELESP 367
QY 337 NLKPVVA--RDVPL--SGFAKADNTLDVTLDTGTPPLVWKVNGSAINIDGRAVVDYV 392
D 368 DTSEVPANLRDVPPEEGGNMDPAPPTDDET--TGRANGQMTINGVF-----SDVENR 420
QY 393 LTONTSEPPGYNIVEVNGADQMSYMLIENDPGAPFTLPHPHLGHDPYVLGRSPDES 452
D 421 LLRNV-----RDVPLMRLNNSNG--WTHFPHILHVDPRVLSRTARG-- 463
QY 453 SNEKHVEDPADAGLISGANPYRDVSMPLPAFGVYLSFRADNPGAMLFCHIAMH---- 508
D 464 -----VEPYEAGLKDQVYMLAREVYVEA-----HYAPFGVYMLHCHNLIHEDHD 510
QY 509 -----VSGGLGVYTLERAD-----LRGAVSDADADDRLCADMRRTPT- 549
D 511 MAAFNVTYLDGYNTTEFTIDPMEPLMRPRPFLIGEPENSGSPSELATDRIOENASF 570
QY 550 NPYPKSD 556
D 571 NPYAQAD 577

```

RESULT 13

```

US-09-942-185-4
; Sequence 4, Application US/09942185
; Patent No. US20020165113A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Convents, Daniel
; APPLICANT: Doornink, Monique
; APPLICANT: van Gastel, Frans
; APPLICANT: Rodrigues, Ana
; APPLICANT: Topozada, Amr
; APPLICANT: De Vries, Cornelis Hendrikus
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: Detergent Compositions Comprising No. US20020165113A1el Phenc
; FILE REFERENCE: C7567
; CURRENT APPLICATION NUMBER: US/09/942,185
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Myrothecium verucaria
US-09-942-185-4

```

```

Query Match 6.5%; Score 204; DB 9; Length 572;
Best Local Similarity 23.4%; Pred. No. 1.3e-09;
Matches 138; Conservative 68; Mismatches 233; Indels 150; Gaps 32;

```

```

QY 23 YEVDSPDTGVVRYPT-----LTLTEVDNMTGPDGVYKVKMLVNNSSIIGPTIFADMGTIQ 78
D 77 YEVE-----IKPETHOYVPLGASAD-LVGTGKSP-----GPTFPVPRGYETV 118
QY 79 VVININLETNGTSLHMHGLHOKGTNLHDG-ANGITTECPITPKGKRYARRKAOYGTSMY 137
D 119 VRFINNAEA-PNSVHLHGSFSRAA--FDGWAEDYTE--PGSPKDYIYFNRQASARTLWY 171
QY 138 HS---HFSAYG-NGVGAIGQINGPA--SLPYTDLDGVFP-----SDYIYSSADELVELT 187

```

```

? TITLE OF INVENTION: LACCASE MUTANTS
? NUMBER OF SEQUENCES: 10
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: No. US20010031490A1o No. US20010031490A1disk of No. US20010031490A1ch
? STREET: 405 Lexington Avenue
? CITY: New York
? STATE: NY
? COUNTRY: USA
? ZIP: 10174
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/732,350
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/032,315
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Rozek, Carol
? REGISTRATION NUMBER: 36,993
? REFERENCE/DOCKET NUMBER: 5200.200-US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-867-0123
? TELEFAX: 212-878-9655
? INFORMATION FOR SEQ. ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 575 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-732-350-8

```

```

Query Match 17.7%; Score 557.5; DB 10; Length 575;
Best Local Similarity 30.9%; Pred. No. 1.1e-39;
Matches 183; Conservative 61; Mismatches 214; Indels 135; Gaps 28;

```

```

QY 44 DNTGPGVYKEMVYNNISITGPIPADMGDTIOVTVINNNLEFN-----GTSIHWHGLH 98
DB 30 DGEIAPDG-VKRNATLVNGGYPGGLIFANKGDTLVKRVONKL-TNPMYRTTSHHGL 87
QY 99 QKGNLHDGANGITCEPIPRGGRKVRFRKA---QOYGTWYSHFSFOYNGVGAIOI 155
DB 88 QHRNADDGSEFYVQCFIV---RESTYTIPLDDGTGTWYHSHLSSQYVDGLRGLVI 144
QY 156 --NGPASPYPYTD--LGVFPISDYSSADEL-----VELTKNSGAPFS-DNVL 199
DB 145 YPKPHRRRLVDVDEKTVLLIIGDWHSSKALLASGNITRQRPVSATINCKGRDPDN-- 202
QY 200 FNGAKRPERGEGEYANVTLPGRNRHLRLINISVENHFOVSLVNHIMCIADMYVNA 259
DB 203 ---TPRNPDT---LYTLKVRGRKRYLRVINSEIASFFPSVEGHVTVYIADGVSTKP 255
QY 260 MTVDLSLGVGORYDVYIEANRFGNFWNV-----TFGGGLCGGSRNP----- 305
DB 256 YQDAFPIIAGQRIDCYEANGDERDYWINAPLNVNKTQALLVYEEERRPRHPKGP 315
QY 306 -----PAALFHY-----AGAPGPPPD--EGKAPV-DHNCLDLPNKKPVARD 345
DB 316 YRKWSEVSEAIKYNHKKHGRGLSGHGLKAKMIEGSHLSRSVYKRONETTVVMD 375
QY 346 -----VPLS---GFA---RRANNTLDVTLDT---TGCTPLFWKYNK-----SAIN 381
DB 376 ESKIVPLEYEGACGSPADIVLDLTGFLNPAIGH---WMINIPYESSKPIPTLKILF 431
QY 382 IDMGRAVDVYLTQNTSFPFGYNIVENVGADQMSYMLIENDPGAFPLPMPMLHGH--D 439
DB 432 DEDQVTSDFKREHYTLPRKNCIEFN-----IKNSGIPIT--HPVHLGHHTWD 480

```

```

QY 440 FYVLGRSPDESPASNERHVEDPADAGILSGANPVRDVSMLPAFGWVLSFRADNPGAW 499
DB 481 VYQGNPNP-----NYNPNRRDVGSTIAG-VRIQFKDNDGPM 519
QY 500 LFCHIAMHVSGLGVYLYLERADDLRGAVSDADAD-DIDRLCADWRRYPTNP 551
DB 520 FLHCHIDMHLEEGFAMVFAEPAEAVKGGPKSVAVDSQMEGICGKRYDMLKSNP 572

```

RESULT 9

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US-09-732-350-4
? Sequence 4, Application US/09732350
? Patent No. US20010031490A1
? GENERAL INFORMATION:
? APPLICANT: Svendsen, Allan
? TITLE OF INVENTION: LACCASE MUTANTS
? NUMBER OF SEQUENCES: 10
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: No. US20010031490A1o No. US20010031490A1disk of No. US20010031490
? STREET: 405 Lexington Avenue
? CITY: New York
? STATE: NY
? COUNTRY: USA
? ZIP: 10174
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/732,350
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/032,315
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Rozek, Carol
? REGISTRATION NUMBER: 36,993
? REFERENCE/DOCKET NUMBER: 5200.200-US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-867-0123
? TELEFAX: 212-878-9655
? INFORMATION FOR SEQ. ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 548 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-732-350-4

```

```

Query Match 17.6%; Score 556; DB 10; Length 548;
Best Local Similarity 31.6%; Pred. No. 1.4e-39;
Matches 162; Conservative 66; Mismatches 195; Indels 90; Gaps 22;

```

```

QY 49 PDGVKREKVMVYNNISITGPIPADMGDTIOVTVINNNLEFN-----SIHHHGHJHOGTN 103
DB 38 PDGFSROAV-LAESVFPGPLLAGKNGDFQINVDEL-TNATMTAKTTTHHGHFGQGTN 95
QY 104 LHDGANGITCEPIPRGGRKVRFRKA---QOYGTWYSHFSFOYNGVGAIOINGPASP 162
DB 96 WADQPARINOCPI-ASGDSFLYNNFOVDPDQGTGTFYHSHLSTQYCDGLRGPPVYVDPAD-P 153
QY 163 Y-----DTDLGVFPISDYSSADELVELTKNSGAPF---SDNVLFGNTAKHPETG--EG 212
DB 154 YLDQYDVDDSTVTTLADWYHTAA-----RLGSPFPADTLLINGLGCRCGACGSPVS 205
QY 213 EVANVTLPGRNRHLRLINISVENHFOVSLVNHIMCIADMYVNAVMYVDSLFLVGOR 272
DB 206 DLANVSTKGRKRYRFRVLSVSCDSFTFFSIDGHSLVNIENVATNHQPLTYDELITTYAGOR 265

```

QY 325 KA-PVDHNCIDLPNLFKPVYARVPLSGFAKRAADNTLDTTGTPLTFVKVNGSALIND 383
 DB 315 NNPDAQINLEADFLALIDPAAPGIPTEG---ADVNLRFQGFSG----- 355
 QY 384 WGAAYVYVLTOMTSPPPGYNIVEVNGADGMS-----YMLIEND-----PGAPFTL 429
 DB 356 -GFTTNGTAYESVPTLIQT--MSGAGSANDLLPAGSVYELPRQGVVELVVPAGVLAG 412
 QY 430 PPHMHLGHDFYLLGKSPDESPASNERHVPDPARDAG--LLSGANPYRVDVSMLEPFG-W 486
 DB 413 PPHFHLHGAFSVY-----RSAGSSYNNVNPVKRQVSLGTYGDE 433
 QY 487 VLSFRADNFGANLFFCHIAMVHSGGLGVYLLERADDLRGAVSDADADLD--RLC 540
 DB 454 VTIREFYDNGPWFHFCHIEFHLMNGIAIVE---AEDMANTV--DANNPVEMAQLC 505

RESULT 5
 US-09-732-350-5
 / Sequence 5, Application US/09732350
 / Patent No. US20010031490A1
 / GENERAL INFORMATION:
 / APPLICANT: Svendsen, Allan
 / TITLE OF INVENTION: LACCASE MUTANTS
 / NUMBER OF SEQUENCES: 10
 / CORRESPONDENCE ADDRESS:
 / STREET: 405 Lexington Avenue
 / CITY: New York
 / STATE: NY
 / COUNTRY: USA
 / ZIP: 10174
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FastSeq for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/732,350
 / FILING DATE:
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 09/032,315
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Rozek, Carol
 / REGISTRATION NUMBER: 36,993
 / REFERENCE/DOCKET NUMBER: 5200.200-US
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 212-867-0123
 / TELEFAX: 212-878-9655
 / INFORMATION FOR SEQ ID NO: 5:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 529 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-09-732-350-5

Query Match 19.3%; Score 609.5; DB 10; Length 529;
 Best Local Similarity 30.3%; Pred. No. 3.8e-44;
 Matches 175; Conservative 73; Mismatches 195; Indels 135; Gaps 24;

QY 25 VDSPTGVVPPYLLTLEVDNMTGPDGVYKEKVLVNSIIGTIFPADMDTIQVYINN 84
 DB 14 VSTPAFAAVANKYFDIKNV--VAPDS-FRSTIVSNGVLPGILIRANKEDTIRINVTQ 70
 QY 85 LE---TNGTSIHMHGILHOKGTLMDGANGITECP-----IPKGGRRVYRFAKQ 130
 DB 71 LTDPMSRRATTIWHGIFQATADEGPAFVTOCPIONLSYTYEILPLRG----- 120

QY 131 QYGTWYSHSHSAQYNGVVAIOI---NGPASIPLYDTD--LGVPFISDYSSADELVE 185
 DB 121 QGTGMVYHAHLAQYVDGLGRLVYIDPNDPHSRVDVDASVYVMEQWYHPPAVLER 180
 QY 186 ---LTKNSG--APPSDNYLFGNATKHPGEGERANVTLP-----GRRHRLINT 232
 DB 181 QMFSTNNLTALLSPVPSGLIN-----GKGRYVGPAVPRSVINWKRKRRLRYLYNA 232
 QY 233 SVENHFOVSLVNTTMCIIADNVYVNAATVDSLEFGVGRYDVVIEANRPGYWFEN--V 290
 DB 233 SAIGSTFTFEGSLIVYIEADGILHOPLAVDSQIYAGQNTSYIVAEJNANTYWRAPR 292
 QY 291 TFGGGLCGGSRNPYPA---ALPHYAGAPGPPTDE-----GRAPYDNCIDLPN----- 337
 DB 293 TVAG---AGTNAMLDPTNVFAVLHYGAPRAEPTTQGSALIGTALVEENLHALINFGAG 349
 QY 338 -----LKPVYARVPLSGFAKRAADNTLDTTGTPLTFVKVNGSALINDGRNAV 389
 DB 350 GSAPADVSLMLAIGRST--VDGILRFTFNNIKYEAPSLPTLLKILANNAS-----NDA 400
 QY 390 DYVLTONTSEPPGYNIYEVN---GADQWSYMLIENDPGAPFTLPPHMLHGHDFY---L 443
 DB 401 DFTPNHETIYLPINKYIELNITGAD-----HHHLHGHTFYKSL 442
 QY 444 GRSPDESPASNERHVPDPARDAGLLSGANPYRVDVSMLEPFGVYLSFRADNFGANLFFHC 503
 DB 443 GGPNNY-----VNPFRDVRVGGTG--VVLRFYDNGPWFHVC 480
 QY 504 HIMVHSGGLGVYLLERADDLRGAVSDADADLD--RLC 540
 DB 481 HIDWHLGALVFAEPQSIKRGVQSVQPPNMMNQLC 518

RESULT 6
 US-09-732-350-3
 / Sequence 3, Application US/09732350
 / Patent No. US20010031490A1
 / GENERAL INFORMATION:
 / APPLICANT: Svendsen, Allan
 / TITLE OF INVENTION: LACCASE MUTANTS
 / NUMBER OF SEQUENCES: 10
 / CORRESPONDENCE ADDRESS:
 / STREET: 405 Lexington Avenue
 / CITY: New York
 / STATE: NY
 / COUNTRY: USA
 / ZIP: 10174
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FastSeq for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/732,350
 / FILING DATE:
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 09/032,315
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Rozek, Carol
 / REGISTRATION NUMBER: 36,993
 / REFERENCE/DOCKET NUMBER: 5200.200-US
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 212-867-0123
 / TELEFAX: 212-878-9655
 / INFORMATION FOR SEQ ID NO: 3:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 499 amino acids
 / TYPE: amino acid

US-09-732-350-10

Query Match 100.0%; Score 3158; DB 10; Length 573;
 Best Local Similarity 100.0%; Pred. No. 66-261;
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 QOSCNTPSNRACWTDGDIINTDYEVDSPTDGVVPRPYTLTLEVDNMTGPDGVKEKVMY 60
DB 1 QOSCNTPSNRACWTDGDIINTDYEVDSPTDGVVPRPYTLTLEVDNMTGPDGVKEKVMY 60
QY 61 NNSIIGPTIFADMGDTIOVYVNNLEFNGTSIHMHGLOKGTNLDGANGITECPPIPKG 120
DB 61 NNSIIGPTIFADMGDTIOVYVNNLEFNGTSIHMHGLOKGTNLDGANGITECPPIPKG 120
QY 121 GRKYRFAKAOQYGTSMTHSFAQYNGVGAIOINGPASLPYDTDLGVPISDIYSSA 180
DB 121 GRKYRFAKAOQYGTSMTHSFAQYNGVGAIOINGPASLPYDTDLGVPISDIYSSA 180
QY 181 DELVELTKNSGAPPSDNLVFNKGAKHETEGEYANVTLPGRHRRLRLINTSVENHFQV 240
DB 181 DELVELTKNSGAPPSDNLVFNKGAKHETEGEYANVTLPGRHRRLRLINTSVENHFQV 240
QY 241 SLVNHMTCITAAQVVPVNAATVDSLEFGVQRYDVYEANRTGNYFNVTFGGGLLCGG 300
DB 241 SLVNHMTCITAAQVVPVNAATVDSLEFGVQRYDVYEANRTGNYFNVTFGGGLLCGG 300
QY 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVVARDVPLSGFAKRAADNTLD 360
DB 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVVARDVPLSGFAKRAADNTLD 360
QY 361 VTLDITGTPTLFWKYNQSAINIDMGRAVVDYVLTONTSPFGGNIYEVNGADQMSYWLIE 420
DB 361 VTLDITGTPTLFWKYNQSAINIDMGRAVVDYVLTONTSPFGGNIYEVNGADQMSYWLIE 420
QY 421 NDGAPFTLPHPHLHGHDYVYLGSRSPESPASNERHVPFAPDAGLLSGANPRRBYSM 480
DB 421 NDGAPFTLPHPHLHGHDYVYLGSRSPESPASNERHVPFAPDAGLLSGANPRRBYSM 480
QY 481 LPAFGWVYLSFRADNPGAMLFCHIAHWYSGGLGVYLLERADDLRGAVSDADADDLRLC 540
DB 481 LPAFGWVYLSFRADNPGAMLFCHIAHWYSGGLGVYLLERADDLRGAVSDADADDLRLC 540
QY 541 ADMRRYWPTRPYPKSDSGLKHRYVEGEMLYKA 573
DB 541 ADMRRYWPTRPYPKSDSGLKHRYVEGEMLYKA 573

```

RESULT 2

US-09-732-350-9

Sequence 9, Application US/09732350
 Patent No. US20010031490A1
 GENERAL INFORMATION:
 APPLICANT: Svendsen, Allan
 APPLICANT: Xu, Feng
 TITLE OF INVENTION: LACCASE MUTANTS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. US20010031490A10 No. US20010031490A1disk of No. US20010031490A1ch
 STREET: 405 Lexington Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10174
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/732,350
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/032,315
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Rokez, Carol
 REGISTRATION NUMBER: 36,993
 REFERENCE/DOCKET NUMBER: 5200.200-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 616 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-732-350-9

Query Match 65.8%; Score 2076.5; DB 10; Length 616;
 Best Local Similarity 66.8%; Pred. No. 76-169;
 Matches 380; Conservative 66; Mismatches 116; Indels 7; Gaps 6;

```

QY 1 QOSCNTPSNRACWTDGDIINTDYEVDSPTDGVVPRPYTLTLEVDNMTGPDGVKEKVMY 60
DB 1 QOSCNTPSNRACWTDGDIINTDYEVDSPTDGVVPRPYTLTLEVDNMTGPDGVKEKVMY 60
QY 61 NNSIIGPTIFADMGDTIOVYVNNLEFNGTSIHMHGLOKGTNLDGANGITECPPIPKG 120
DB 61 NNSIIGPTIFADMGDTIOVYVNNLEFNGTSIHMHGLOKGTNLDGANGITECPPIPKG 120
QY 107 NDRLGTPVFAVWMDTTEVYVNNHRTNGTSIHMHGLOKGTNLDGANGITECPPIPKG 165
DB 107 NDRLGTPVFAVWMDTTEVYVNNHRTNGTSIHMHGLOKGTNLDGANGITECPPIPKG 165
QY 121 GRKYRFAKAOQYGTSMTHSFAQYNGVGAIOINGPASLPYDTDLGVPISDIYSSA 180
DB 121 GRKYRFAKAOQYGTSMTHSFAQYNGVGAIOINGPASLPYDTDLGVPISDIYSSA 180
QY 166 GSRYVSPRFAQYGTSMTHSFAQYNGVGAIOINGPASLPYDTDLGVPISDIYSSA 225
DB 166 GSRYVSPRFAQYGTSMTHSFAQYNGVGAIOINGPASLPYDTDLGVPISDIYSSA 225
QY 181 DELVELTKNSGAPPSDNLVFNKGAKHETEGEYANVTLPGRHRRLRLINTSVENHFQ 239
DB 181 DELVELTKNSGAPPSDNLVFNKGAKHETEGEYANVTLPGRHRRLRLINTSVENHFQ 239
QY 226 DQVLETLKNGAPPSDNLVFNKGAKHETEGEYANVTLPGRHRRLRLINTSVENHFQ 285
DB 226 DQVLETLKNGAPPSDNLVFNKGAKHETEGEYANVTLPGRHRRLRLINTSVENHFQ 285
QY 240 VSLVNHMTCITAAQVVPVNAATVDSLEFGVQRYDVYEANRTGNYFNVTFGGGLLCGG 299
DB 240 VSLVNHMTCITAAQVVPVNAATVDSLEFGVQRYDVYEANRTGNYFNVTFGGGLLCGG 299
QY 286 VSLAKHMTVYLAQVVPVNAATVDSLEFGVQRYDVYEANRTGNYFNVTFGGGLLCGG 345
DB 286 VSLAKHMTVYLAQVVPVNAATVDSLEFGVQRYDVYEANRTGNYFNVTFGGGLLCGG 345
QY 300 GSRRPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVVARDVPLSGFAKRAADNTLD 359
DB 300 GSRRPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLNLRPVVARDVPLSGFAKRAADNTLD 359
QY 346 FSHNPAALFIRYEGADALPTDGAAPKDHQCIDTLSPVQKVPVQGFVPEPNTL 405
DB 346 FSHNPAALFIRYEGADALPTDGAAPKDHQCIDTLSPVQKVPVQGFVPEPNTL 405
QY 360 DVTL--DTTGP--LFWKYNQSAINIDMGRAVVDYVLTONTSPFGGNIYEVNGADQMS 415
DB 360 DVTL--DTTGP--LFWKYNQSAINIDMGRAVVDYVLTONTSPFGGNIYEVNGADQMS 415
QY 406 PVLHVDQAAAPHVFTWKINGSDADVDMDRVLLEYVANNNDLSIPVKNNTIVRVDGVNEWT 465
DB 406 PVLHVDQAAAPHVFTWKINGSDADVDMDRVLLEYVANNNDLSIPVKNNTIVRVDGVNEWT 465
QY 416 YWLENDPGAPFTLPHPHLHGHDYVYLGSRSPESPASNERHVPFAPDAGLLSGANPRRBYSM 475
DB 416 YWLENDPGAPFTLPHPHLHGHDYVYLGSRSPESPASNERHVPFAPDAGLLSGANPRRBYSM 475
QY 466 YWLENDPEGRSLPHPHLHGHDYVYLGSRSPESPASNERHVPFAPDAGLLSGANPRRBYSM 525
DB 466 YWLENDPEGRSLPHPHLHGHDYVYLGSRSPESPASNERHVPFAPDAGLLSGANPRRBYSM 525
QY 476 RDSVMDPAFGWVYLSFRADNPGAMLFCHIAHWYSGGLGVYLLERADDLRGAVSDADADD 535
DB 476 RDSVMDPAFGWVYLSFRADNPGAMLFCHIAHWYSGGLGVYLLERADDLRGAVSDADADD 535
QY 526 RDTYMLPARFGLVLAFTDNDGAMLFCHIAHWYSGGLGVYLLERADDLRGAVSDADADD 585
DB 526 RDTYMLPARFGLVLAFTDNDGAMLFCHIAHWYSGGLGVYLLERADDLRGAVSDADADD 585
QY 536 LDRICADMRRYWPTRPYPKSDSGLKHRYVEGEMLYKA 563
DB 536 LDRICADMRRYWPTRPYPKSDSGLKHRYVEGEMLYKA 563
QY 586 LERVCREMKDWEAKSPHGKIDSGLKRWR 614
DB 586 LERVCREMKDWEAKSPHGKIDSGLKRWR 614

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RESULT 3

US-09-732-350-2

Sequence 2, Application US/09732350
 Patent No. US20010031490A1
 GENERAL INFORMATION:
 APPLICANT: Svendsen, Allan
 APPLICANT: Xu, Feng
 TITLE OF INVENTION: LACCASE MUTANTS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:

DB 228 DELVELTKNSGAFSDNVLENGTAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQY 287
QY 241 SLVNHMTCTIADMTVPVNAATVDSLEFLGVRDYVIEANRTPGNWENYTFGGGLCG 300
DB 288 SLVNHMTCTIADMTVPVNAATVDSLEFLGVRDYVIEANRTPGNWENYTFGGGLCG 347
QY 301 SRNPYPAALFHYAGAPGPTDEGKAPVDHNCIDLPLKPVVARDVPLSGFAKADNTLD 360
DB 348 SRNPYPAALFHYAGAPGPTDEGKAPVDHNCIDLPLKPVVARDVPLSGFAKADNTLD 407
QY 361 VILDTGTGTLFVWKVNGSAINIDMGRAVDYVLTONTSPFPNGIYEVNCAQDWSTWLE 420
DB 408 VILDTGTGTLFVWKVNGSAINIDMGRAVDYVLTONTSPFPNGIYEVNCAQDWSTWLE 467
QY 421 NDGAFPTLPHPMLHGHDFYVYLGSRPDESASNERHVPDPADAGLLSGANFVRDYSM 480
DB 468 NDGAFPTLPHPMLHGHDFYVYLGSRPDESASNERHVPDPADAGLLSGANFVRDYSM 527
QY 481 LPAFGWVLSFRADNPGAMLFCHIAMHVSGLGVYVYLERADDLRGAVSDADADDLRLC 540
DB 528 LPAFGWVLSFRADNPGAMLFCHIAMHVSGLGVYVYLERADDLRGAVSDADADDLRLC 587
QY 541 ADMRRYPTNPYPKSDSGLKHRRVEGEMLYKA 573
DB 588 ADMRRYPTNPYPKSDSGLKHRRVEGEMLYKA 620

RESULT 15
US-08-749-882A-2
; Sequence 2, Application US/08749882A
; Patent No. 5750388
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy
; APPLICANT: Thompson, Sheryl
; APPLICANT: Xu, Peng
; TITLE OF INVENTION: Purified Scytalidium laccases
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57503880 No. 5750388disk Of No. 5750388th America, Inc.
; STREET: 405 Lexington Avenue - 64th Fl.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,882A
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4186,020-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-878-9652
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 616 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE: Scytalidium thermophilum
; ORGANISM: Scytalidium thermophilum
US-08-749-882A-2

Query Match

66.2%; Score 2089.5; DB 1; length 616;

Best Local Similarity 67.0%; Pred. No. 56-189;
Matches 381; Conservative 66; Mismatches 115; Indels 7; Gaps 6;
QY 1 QSCNTPSNRACCTDGYDINDTDEVDSPOTGVYRPTLLILEDMNTGPDGVYKEVMY 60
DB 47 QGCHSPSNRACWCSCGFINTDYEKTPTNPGVRRRTFTITVDNPNRPGDGVYKEVMY 106
QY 61 NSIIGPTTFADWGTIOYTVINNLNETNGSTIHWGILHOKGTLLHKGANGITCECP1PPK 120
DB 107 NDKLGPPTVPAKNGDTIETVANNHNTNGSTIHWGILHOKGTLLHKGANGITCECP1PPK 165
QY 121 GRRVYRPAKQOYGTSWYSHFSAYQNGVGAIOINGPASPYPDTDLGVFPISDYYS 180
DB 166 GSRVYSEFRARQYGTSWYSHFSAYQNGVGAIOINGPASPYPDTDLGVFPISDYYS 225
QY 181 DELV-ELTKNSGAFSDNVLENGTAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQY 239
DB 226 DQVLETKNSGAFSDNVLENGTAKHPETGESEYANVTLPGRHRRLRLINTSVENHFQY 285
QY 240 VSLVNHMTCTIADMTVPVNAATVDSLEFLGVRDYVIEANRTPGNWENYTFGGGLCG 299
DB 286 VSLVNHMTCTIADMTVPVNAATVDSLEFLGVRDYVIEANRTPGNWENYTFGGGLCG 345
QY 300 GSRNPYPAALFHYAGAPGPTDEGKAPVDHNCIDLPLKPVVARDVPLSGFAKADNTLD 359
DB 346 FSHNPAPPAALFHYAGAPGPTDEGKAPVDHNCIDLPLKPVVARDVPLSGFAKADNTLD 405
QY 360 DVTLL-DTGTGTLFVWKVNGSAINIDMGRAVDYVLTONTSPFPNGIYEVNCAQDW 415
DB 406 DVTLL-DTGTGTLFVWKVNGSAINIDMGRAVDYVLTONTSPFPNGIYEVNCAQDW 465
QY 416 YMLIENDPGAPFTLPHPMLHGHDFYVYLGSRPDESASNERHVPDPADAGLLSGANFVR 475
DB 466 YMLIENDPGAPFTLPHPMLHGHDFYVYLGSRPDESASNERHVPDPADAGLLSGANFVR 525
QY 476 RDVSMPLPAGWVLSFRADNPGAMLFCHIAMHVSGLGVYVYLERADDLRGAVSDADADD 535
DB 526 RDVSMPLPAGWVLSFRADNPGAMLFCHIAMHVSGLGVYVYLERADDLRGAVSDADADD 585
QY 536 LDRLCADMRRYPTNPYPKSDSGLKHRRVEGEMLYKA 563
DB 586 LDRLCADMRRYPTNPYPKSDSGLKHRRVEGEMLYKA 614

Search completed: December 4, 2002, 10:48:03
Job time : 19 secs

TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Myceliophthora thermophila
 PCT-US95-06815-2

Query Match 100.0%; Score 3158; DB 5; Length 620;
 Best Local Similarity 100.0%; Pred. No. 4e-290;
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSCNTPSRACWTDGDIYDITDEVDSPDGVVRYPTLTLEVDNMTGPGGVYKEMV 60
 DB 48 QOSCNTPSRACWTDGDIYDITDEVDSPDGVVRYPTLTLEVDNMTGPGGVYKEMV 107
 QY 61 NNSIIGPTIFADMGDTIOYVINNLETNGTSIMHGLHOKGTNLHDANGITTECPPIPKG 120
 DB 108 NNSIIGPTIFADMGDTIOYVINNLETNGTSIMHGLHOKGTNLHDANGITTECPPIPKG 167
 QY 121 GRKVRPKAQQYGTSMYSHFSAQYNGVGAIOINGPASTPYDTDLGVFPISDYSSA 180
 DB 168 GRKVRPKAQQYGTSMYSHFSAQYNGVGAIOINGPASTPYDTDLGVFPISDYSSA 227
 QY 181 DELVELTKNSGAPSDNVLEFNGTAKHPETGEGEYANVTLPGRHRRLRLINTSVENHFQY 240
 DB 228 DELVELTKNSGAPSDNVLEFNGTAKHPETGEGEYANVTLPGRHRRLRLINTSVENHFQY 287
 QY 241 SLVNHMTCTIADVPVNAATVDSLEFLVGQRYDVVLEARNTPGNVFNTPFGGILLCGG 300
 DB 288 SLVNHMTCTIADVPVNAATVDSLEFLVGQRYDVVLEARNTPGNVFNTPFGGILLCGG 347
 QY 301 SRNPYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPVVARDVPLSGFAKRAADTLD 360
 DB 348 SRNPYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPVVARDVPLSGFAKRAADTLD 407
 QY 361 VTLDTGTFLEFVKVNGSAINIDMGRAVDVYLTQNTSPPGYINIVVNGADQMSYVLE 420
 DB 408 VTLDTGTFLEFVKVNGSAINIDMGRAVDVYLTQNTSPPGYINIVVNGADQMSYVLE 467
 QY 421 NDGAPFTLPHPMHLHGHDYVILGRSPDESPASNERHVPDPADAGLLSGANPVRDYSM 480
 DB 468 NDGAPFTLPHPMHLHGHDYVILGRSPDESPASNERHVPDPADAGLLSGANPVRDYSM 527
 QY 481 LPAFGVVLVSFRADNPGAMLFCHIAHVSGLGVYVLEADDLRGAVSDADDDRLC 540
 DB 528 LPAFGVVLVSFRADNPGAMLFCHIAHVSGLGVYVLEADDLRGAVSDADDDRLC 587
 QY 541 ADMRRYPTNPYPKSDSGLKHRRVEEGEMLVKA 573
 DB 588 ADMRRYPTNPYPKSDSGLKHRRVEEGEMLVKA 620

RESULT 12
 US-08-940-661A-2
 Sequence 2, Application US/08940661A
 Patent No. 5795760

GENERAL INFORMATION:
 APPLICANT: BERKA, Randy Michael
 APPLICANT: BROWN, Stephen H.
 APPLICANT: XU, Feng
 APPLICANT: SCHNEIDER, Palle
 APPLICANT: OXENB LL, Karen M.
 APPLICANT: MASLYNG, Dorrit A.
 TITLE OF INVENTION: PURIFIED MYCELIOPHTHORA LACCASES AND NUCLEIC
 ACIDS
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 57957600 No. 5795760disk of No. 5795760th America, Inc.
 STREET: 405 Lexington Avenue, 64th Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/940,661A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/441,146
 FILING DATE: 15-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Harrington, James J.
 REGISTRATION NUMBER: 38,711
 REFERENCE/DOCKET NUMBER: 4184.010-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 620 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-940-661A-2

Query Match 99.0%; Score 3127; DB 1; Length 620;
 Best Local Similarity 99.0%; Pred. No. 3.5e-287;
 Matches 567; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QOSCNTPSRACWTDGDIYDITDEVDSPDGVVRYPTLTLEVDNMTGPGGVYKEMV 60
 DB 48 QOSCNTPSRACWTDGDIYDITDEVDSPDGVVRYPTLTLEVDNMTGPGGVYKEMV 107
 QY 61 NNSIIGPTIFADMGDTIOYVINNLETNGTSIMHGLHOKGTNLHDANGITTECPPIPKG 120
 DB 108 NNSIIGPTIFADMGDTIOYVINNLETNGTSIMHGLHOKGTNLHDANGITTECPPIPKG 167
 QY 121 GRKVRPKAQQYGTSMYSHFSAQYNGVGAIOINGPASTPYDTDLGVFPISDYSSA 180
 DB 168 GRKVRPKAQQYGTSMYSHFSAQYNGVGAIOINGPASTPYDTDLGVFPISDYSSA 227
 QY 181 DELVELTKNSGAPSDNVLEFNGTAKHPETGEGEYANVTLPGRHRRLRLINTSVENHFQY 240
 DB 228 DELVELTKNSGAPSDNVLEFNGTAKHPETGEGEYANVTLPGRHRRLRLINTSVENHFQY 287
 QY 241 SLVNHMTCTIADVPVNAATVDSLEFLVGQRYDVVLEARNTPGNVFNTPFGGILLCGG 300
 DB 288 SLVNHMTCTIADVPVNAATVDSLEFLVGQRYDVVLEARNTPGNVFNTPFGGILLCGG 347
 QY 301 SRNPYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPVVARDVPLSGFAKRAADTLD 360
 DB 348 SRNPYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPVVARDVPLSGFAKRAADTLD 407
 QY 361 VTLDTGTFLEFVKVNGSAINIDMGRAVDVYLTQNTSPPGYINIVVNGADQMSYVLE 420
 DB 408 VTLDTGTFLEFVKVNGSAINIDMGRAVDVYLTQNTSPPGYINIVVNGADQMSYVLE 467
 QY 421 NDGAPFTLPHPMHLHGHDYVILGRSPDESPASNERHVPDPADAGLLSGANPVRDYSM 480
 DB 468 NDGAPFTLPHPMHLHGHDYVILGRSPDESPASNERHVPDPADAGLLSGANPVRDYSM 527
 QY 481 LPAFGVVLVSFRADNPGAMLFCHIAHVSGLGVYVLEADDLRGAVSDADDDRLC 540
 DB 528 LPAFGVVLVSFRADNPGAMLFCHIAHVSGLGVYVLEADDLRGAVSDADDDRLC 587
 QY 541 ADMRRYPTNPYPKSDSGLKHRRVEEGEMLVKA 573
 DB 588 ADMRRYPTNPYPKSDSGLKHRRVEEGEMLVKA 620

RESULT 13
 US-09-083-485-2


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,281
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,318
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Greeng, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-576-281-10
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Query Match 100.0%; Score 3158; DB 4; Length 573;
Best Local Similarity 100.0%; Pred. No. 3.6e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QOSCNTPSNRACWTDGYDINTDYEVDSPTDGVVRYTLTLEVDNMTGPDGVVEKVMY 60
DB 1 QOSCNTPSNRACWTDGYDINTDYEVDSPTDGVVRYTLTLEVDNMTGPDGVVEKVMY 60
QY 61 NNSLTGPTIRADMGDTIQVYVNNLENTGSIHMHGKHOKGTNLDHANGITTECPPIPKG 120
DB 61 NNSLTGPTIRADMGDTIQVYVNNLENTGSIHMHGKHOKGTNLDHANGITTECPPIPKG 120
QY 121 GRKYRRAKAOYGTSMYSHFSAOYGVNGVGAIOINGPASPYPDTDLGVPFISDYSSA 180
DB 121 GRKYRRAKAOYGTSMYSHFSAOYGVNGVGAIOINGPASPYPDTDLGVPFISDYSSA 180
QY 181 DEVELTKNSGAPSDNVLENGTAKHPTGEGEYANTLTGRRHRLRLINTSVENHFOY 240
DB 181 DEVELTKNSGAPSDNVLENGTAKHPTGEGEYANTLTGRRHRLRLINTSVENHFOY 240
QY 241 SLVNHMCIIAADMVPPNATVDSLEFLVGQRDVVLEANTPGNYFNVTFFGGLLCGG 300
DB 241 SLVNHMCIIAADMVPPNATVDSLEFLVGQRDVVLEANTPGNYFNVTFFGGLLCGG 300
QY 301 SRNYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVADVPLSGFAKRAADNTLD 360
DB 301 SRNYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVADVPLSGFAKRAADNTLD 360
QY 361 VTLDTGTPLTFVWKVNGSAINIDMGRAVVDVLTQNTSFPFGYNIIVEVNGADQMSYMLE 420
DB 361 VTLDTGTPLTFVWKVNGSAINIDMGRAVVDVLTQNTSFPFGYNIIVEVNGADQMSYMLE 420
QY 421 NDGPAPTLPHMLHGHDFVLGRSPDESPASNERHVEDARAGLLSGANPRRQVSM 480
DB 421 NDGPAPTLPHMLHGHDFVLGRSPDESPASNERHVEDARAGLLSGANPRRQVSM 480
QY 481 LPAIGWVVLSEFRADNPGAMLEFHCHIAHVSGLGVYLLERADDLGAVSDADADDLRLC 540
DB 481 LPAIGWVVLSEFRADNPGAMLEFHCHIAHVSGLGVYLLERADDLGAVSDADADDLRLC 540
QY 541 ADMRRYPTNPKSDGSLKRWVEEGEMLVKA 573
DB 541 ADMRRYPTNPKSDGSLKRWVEEGEMLVKA 573
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RESULT 9

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US-08-706-037-27
Sequence 27, Application US/08706037
Patent No. 5770419
GENERAL INFORMATION:
APPLICANT: Xu, Feng
APPLICANT: Beika, Randy M.
APPLICANT: Wahlechner, Jill A.
TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5770419 No. 5770419disk of No. 5770419th America, Inc.
STREET: 405 Lexington Avenue, 64th floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,037
FILING DATE: 30-Aug-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,800
FILING DATE: 1-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4526.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-706-037-27
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Query Match 100.0%; Score 3158; DB 1; Length 620;
Best Local Similarity 100.0%; Pred. No. 4e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QOSCNTPSNRACWTDGYDINTDYEVDSPTDGVVRYTLTLEVDNMTGPDGVVEKVMY 60
DB 48 QOSCNTPSNRACWTDGYDINTDYEVDSPTDGVVRYTLTLEVDNMTGPDGVVEKVMY 107
QY 61 NNSLTGPTIRADMGDTIQVYVNNLENTGSIHMHGKHOKGTNLDHANGITTECPPIPKG 120
DB 108 NNSLTGPTIRADMGDTIQVYVNNLENTGSIHMHGKHOKGTNLDHANGITTECPPIPKG 167
QY 121 GRKYRRAKAOYGTSMYSHFSAOYGVNGVGAIOINGPASPYPDTDLGVPFISDYSSA 180
DB 168 GRKYRRAKAOYGTSMYSHFSAOYGVNGVGAIOINGPASPYPDTDLGVPFISDYSSA 227
QY 181 DEVELTKNSGAPSDNVLENGTAKHPTGEGEYANTLTGRRHRLRLINTSVENHFOY 240
DB 228 DEVELTKNSGAPSDNVLENGTAKHPTGEGEYANTLTGRRHRLRLINTSVENHFOY 287
QY 241 SLVNHMCIIAADMVPPNATVDSLEFLVGQRDVVLEANTPGNYFNVTFFGGLLCGG 300
DB 288 SLVNHMCIIAADMVPPNATVDSLEFLVGQRDVVLEANTPGNYFNVTFFGGLLCGG 347
QY 301 SRNYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVADVPLSGFAKRAADNTLD 360
DB 348 SRNYPALIFHYAGAPGPTDEGKAPVDHNCIDLPLKPYVADVPLSGFAKRAADNTLD 407
QY 361 VTLDTGTPLTFVWKVNGSAINIDMGRAVVDVLTQNTSFPFGYNIIVEVNGADQMSYMLE 420
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QY 541 ADMRRYPTNPKSDSGLKHRRVEEGEWLYKA 573
DB 541 ADMRRYPTNPKSDSGLKHRRVEEGEWLYKA 573

RESULT 5
US-09-399-866-10
Sequence 10, Application US/09399886
Patent No. 6140092
GENERAL INFORMATION:
APPLICANT: Pedersen, Anders
APPLICANT: Svendsen, Allan
APPLICANT: Schneider, Palle
APPLICANT: Rasmussen, Grethe
APPLICANT: Cherry, Joel
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61400920 No. 6140092disk of No. 61400922th America
STREET: 405 Lexington Avenue
CITY: New York
COUNTRY: USA
ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/399,886
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,318
FILING DATE: December 18, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-399-866-10

Query Match 100.0%; Score 3158; DB 4; Length 573;
Best Local Similarity 100.0%; Pred. No. 3.6e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSCNTPSNRACWTGDIINTDYEVDSPDTGVVRYPTLTLEVDNMTGPDGVYKEMVLY 60
DB 1 QOSCNTPSNRACWTGDIINTDYEVDSPDTGVVRYPTLTLEVDNMTGPDGVYKEMVLY 60

QY 61 NNSIIGPTTFADMGDTIQTVINNLSTNGTSHMHGLHOKGTLNLDGANGITTECPIDPKG 120
DB 61 NNSIIGPTTFADMGDTIQTVINNLSTNGTSHMHGLHOKGTLNLDGANGITTECPIDPKG 120

QY 121 GKKVYRFAKQOYGTSWYSHFSAOYGNVYGAIOINGPASTLPYDTDLGVPEPIDYYSSA 180
DB 121 GKKVYRFAKQOYGTSWYSHFSAOYGNVYGAIOINGPASTLPYDTDLGVPEPIDYYSSA 180

QY 181 DELVELTKNSGAFSDNVLFNGTAKHPETGECEYANVTLPGRHRRLRLINTSEVNHFOY 240
DB 181 DELVELTKNSGAFSDNVLFNGTAKHPETGECEYANVTLPGRHRRLRLINTSEVNHFOY 240

QY 241 SLVNHMCIADAMVPMVNMATVDSLFLGVGQRDVIYIENRTGNTWPNVTFGGGLCGG 300

DB 241 SLVNHMCIADAMVPMVNMATVDSLFLGVGQRDVIYIENRTGNTWPNVTFGGGLCGG 300
QY 301 SRNYPFAIFHYAGAPGPPIDEKAPVDHNCIDLPMUKRYVAVDVLSGFAKADTLLD 360
DB 301 SRNYPFAIFHYAGAPGPPIDEKAPVDHNCIDLPMUKRYVAVDVLSGFAKADTLLD 360

QY 361 VTLDTTCTPLFVWKVNSAINIDMGRAVVDVLTQNTSPPGGYIVVNGADOMSYLIE 420
DB 361 VTLDTTCTPLFVWKVNSAINIDMGRAVVDVLTQNTSPPGGYIVVNGADOMSYLIE 420

QY 421 NDCGAPPTLPHMLHGHDFYVLGRSPDES PASNERHVPDPADAGLLSGANPYRDVSM 480
DB 421 NDCGAPPTLPHMLHGHDFYVLGRSPDES PASNERHVPDPADAGLLSGANPYRDVSM 480

QY 481 LPAGWVLSFRADNPANLFEHCIAHHVSGGLGVYLLERADDLRGAVSDADDLRLC 540
DB 481 LPAGWVLSFRADNPANLFEHCIAHHVSGGLGVYLLERADDLRGAVSDADDLRLC 540

QY 541 ADMRRYPTNPKSDSGLKHRRVEEGEWLYKA 573
DB 541 ADMRRYPTNPKSDSGLKHRRVEEGEWLYKA 573

RESULT 6
US-09-396-260-10
Sequence 10, Application US/09396260
Patent No. 6184015
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Xu, Feng
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61840150 No. 6184015disk of No. 6184015th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/396,260
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/032,315
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 573 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-396-260-10

Query Match 100.0%; Score 3158; DB 4; Length 573;
Best Local Similarity 100.0%; Pred. No. 3.6e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSCNTPSNRACWTGDIINTDYEVDSPDTGVVRYPTLTLEVDNMTGPDGVYKEMVLY 60

```

Db 1 QOQCNTPSNRACWTGDIINTDYEVDSPTDGVVRPTLTLEVDNMTGPGGVKEXMVLV 60
QY 61 NNSIIGFTTFADMGDTIQVTVINNNLETNGTSIMHGHGKGTMLHDGANGITECP1PPKG 120
Db 61 NNSIIGFTTFADMGDTIQVTVINNNLETNGTSIMHGHGKGTMLHDGANGITECP1PPKG 120
QY 121 GRRVYRKAQOYGTSMYHSFSAQYGVGAIOINGPASP1PYDTDLGVPPISDYSSA 180
Db 121 GRRVYRKAQOYGTSMYHSFSAQYGVGAIOINGPASP1PYDTDLGVPPISDYSSA 180
QY 181 DELVELTKNSGAPFSDNVLENGTAKHPETGEGETANVTLPGRHRRLRLINTSVENHFQY 240
Db 181 DELVELTKNSGAPFSDNVLENGTAKHPETGEGETANVTLPGRHRRLRLINTSVENHFQY 240
QY 241 SLVNHMCIITADMPVPMNATVDSLFLGVGQRYDVYEANRTPGNVTFFGGGLCGG 300
Db 241 SLVNHMCIITADMPVPMNATVDSLFLGVGQRYDVYEANRTPGNVTFFGGGLCGG 300
QY 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLMKPVADVP1LSGFARADNTLD 360
Db 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLMKPVADVP1LSGFARADNTLD 360
QY 361 VTLDTGTPLFVWKVNGSAINIDMGRAVVDYVLTONTSPPGYNIYEVDGADQMSYWLIE 420
Db 361 VTLDTGTPLFVWKVNGSAINIDMGRAVVDYVLTONTSPPGYNIYEVDGADQMSYWLIE 420
QY 421 NDGAPFTLPHPMLHGHDPYV1GRSPDESPASNERHVPDPADAG1LSGANVPRDYSM 480
Db 421 NDGAPFTLPHPMLHGHDPYV1GRSPDESPASNERHVPDPADAG1LSGANVPRDYSM 480
QY 481 LPAFGWVLSFRADNPGAMLFHCHIAMHVSGLGVYVLEADDLRGAVSPADADDDRLC 540
Db 481 LPAFGWVLSFRADNPGAMLFHCHIAMHVSGLGVYVLEADDLRGAVSPADADDDRLC 540
QY 541 ADMRRYPTNPYKSDSG1KHRVVEGEMLVKA 573
Db 541 ADMRRYPTNPYKSDSG1KHRVVEGEMLVKA 573

```

RESULT 2

```

US-09-032-315-10
; Sequence 10, Application US/09032315
; Patent No. 5985818
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59858180 No. 5985818disk of No. 5985818th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032, 315
; FILING DATE: 27-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rorek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200, 200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-032-315-10

```

```

Query Match 100.0%; Score 3158; DB 2; Length 573;
Best Local Similarity 100.0%; Pred. No. 3, 6e-290;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QOQCNTPSNRACWTGDIINTDYEVDSPTDGVVRPTLTLEVDNMTGPGGVKEXMVLV 60
Db 1 QOQCNTPSNRACWTGDIINTDYEVDSPTDGVVRPTLTLEVDNMTGPGGVKEXMVLV 60
QY 61 NNSIIGFTTFADMGDTIQVTVINNNLETNGTSIMHGHGKGTMLHDGANGITECP1PPKG 120
Db 61 NNSIIGFTTFADMGDTIQVTVINNNLETNGTSIMHGHGKGTMLHDGANGITECP1PPKG 120
QY 121 GRRVYRKAQOYGTSMYHSFSAQYGVGAIOINGPASP1PYDTDLGVPPISDYSSA 180
Db 121 GRRVYRKAQOYGTSMYHSFSAQYGVGAIOINGPASP1PYDTDLGVPPISDYSSA 180
QY 181 DELVELTKNSGAPFSDNVLENGTAKHPETGEGETANVTLPGRHRRLRLINTSVENHFQY 240
Db 181 DELVELTKNSGAPFSDNVLENGTAKHPETGEGETANVTLPGRHRRLRLINTSVENHFQY 240
QY 241 SLVNHMCIITADMPVPMNATVDSLFLGVGQRYDVYEANRTPGNVTFFGGGLCGG 300
Db 241 SLVNHMCIITADMPVPMNATVDSLFLGVGQRYDVYEANRTPGNVTFFGGGLCGG 300
QY 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLMKPVADVP1LSGFARADNTLD 360
Db 301 SRNPYPAIFHYAGAPGPTDEGKAPVDHNCIDLPLMKPVADVP1LSGFARADNTLD 360
QY 361 VTLDTGTPLFVWKVNGSAINIDMGRAVVDYVLTONTSPPGYNIYEVDGADQMSYWLIE 420
Db 361 VTLDTGTPLFVWKVNGSAINIDMGRAVVDYVLTONTSPPGYNIYEVDGADQMSYWLIE 420
QY 421 NDGAPFTLPHPMLHGHDPYV1GRSPDESPASNERHVPDPADAG1LSGANVPRDYSM 480
Db 421 NDGAPFTLPHPMLHGHDPYV1GRSPDESPASNERHVPDPADAG1LSGANVPRDYSM 480
QY 481 LPAFGWVLSFRADNPGAMLFHCHIAMHVSGLGVYVLEADDLRGAVSPADADDDRLC 540
Db 481 LPAFGWVLSFRADNPGAMLFHCHIAMHVSGLGVYVLEADDLRGAVSPADADDDRLC 540
QY 541 ADMRRYPTNPYKSDSG1KHRVVEGEMLVKA 573
Db 541 ADMRRYPTNPYKSDSG1KHRVVEGEMLVKA 573

RESULT 3
US-08-993-318A-10
; Sequence 10, Application US/08993318A
; Patent No. 5998353
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59983530 No. 5998353disk of No. 5998353th America
; STREET: 405 Lexington Avenue
; CITY: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

PT oxidation potential - or altered pH optimum, or mediator or
 PT oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting
 PT dye transfer and in bleaching textiles, especially as detergent
 PT additive
 PS Claim 15; Page -: 147pp; English.

XX The present sequence represents a mutant laccase protein. The
 CC specification describes active laccase variants (see AAM76282,
 CC AAM76296-99 and AAM76316-17) having increased oxidation potential,
 CC altered pH optimum, altered mediator and/or altered oxygen/hydroxide
 CC ion pathway. The laccase variants are used specifically to oxidise
 CC substrates, to inhibit dye transfer, and for bleaching textiles,
 CC specifically denim. They can also be used for lignin modification,
 CC strengthening paper, polymerisation of phenols, dyeing of hair and
 CC textiles and waste water treatment.
 CC note: the present sequence does not appear in the specification; it was
 CC constructed using information provided.

XX Sequence 573 AA;

Query Match Best Local Similarity 98.5%; Score 3112; DB 19; Length 573;

Matches 555; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 QQSCNTPSNRACWTDGIDTIDYEDSPDTGVVRYPTLTLEVDNMTGPDGVYKEMV 60
 DB 1 QQSCNTPSNRACWTDGIDTIDYEDSPDTGVVRYPTLTLEVDNMTGPDGVYKEMV 60
 QY 61 NNSIIGPTFADMGDTIQVYVNNLENGTSHMHGILHOGKTNLHOGANKITECP1PPKG 120
 DB 61 NNSIIGPTFADMGDTIQVYVNNLENGTSHMHGILHOGKTNLHOGANKITECP1PPKG 120
 QY 121 GRKYRFRKAQOYGTSMYSHFSAOYGVYGAIOINGPASTLPDITDGLGVPISDYSSA 180
 DB 121 GRKYRFRKAQOYGTSMYSHFSAOYGVYGAIOINGPASTLPDITDGLGVPISDYSSA 180
 QY 121 GRKYRFRKAQOYGTSMYSHFSAOYGVYGAIOINGPASTLPDITDGLGVPISDYSSA 180
 DB 121 GRKYRFRKAQOYGTSMYSHFSAOYGVYGAIOINGPASTLPDITDGLGVPISDYSSA 180
 QY 181 DELVELTKNSGAPFSDNVLEFNGTAKHPETGEGETAVNTLTPGRHRRLRLINTSEVNHFOV 240
 DB 181 DELVELTKNSGAPFSDNVLEFNGTAKHPETGEGETAVNTLTPGRHRRLRLINTSEVNHFOV 240
 QY 181 DELVELTKNSGAPFSDNVLEFNGTAKHPETGEGETAVNTLTPGRHRRLRLINTSEVNHFOV 240
 DB 181 DELVELTKNSGAPFSDNVLEFNGTAKHPETGEGETAVNTLTPGRHRRLRLINTSEVNHFOV 240
 QY 241 SLVNHMTCTIAADMVNPVNAATVDSLPLGVGQRDVYIENKRTGNTVFNTPFGGLCGG 300
 DB 241 SLVNHMTCTIAADMVNPVNAATVDSLPLGVGQRDVYIENKRTGNTVFNTPFGGLCGG 300
 QY 301 SRNPYPAIIFHYAGAPGPTDEKAPVDHNCIDLPLKRVVADVPLSGFAKRAVDTLTD 360
 DB 301 SRNPYPAIIFHYAGAPGPTDEKAPVDHNCIDLPLKRVVADVPLSGFAKRAVDTLTD 360
 QY 361 VILDTGTPTLFPVKVNGSAINIDMGRAVDVYLTQNTSPPPGYNIVEVNGADQMSYWLIE 420
 DB 361 VILDTGTPTLFPVKVNGSAINIDMGRAVDVYLTQNTSPPPGYNIVEVNGADQMSYWLIE 420
 QY 421 NDGAPPTLPHPHLHGHDYVVLGRSPDESASNERHVPPAPADAGLLSGANVRRDYSM 480
 DB 421 NDGAPPTLPHPHLHGHDYVVLGRSPDESASNERHVPPAPADAGLLSGANVRRDYSM 480
 QY 481 LPAFGVWVLSFRADNPGAMLFCHIHAMVSGGLGVVYLERADDLRGASVADADDDRLC 540
 DB 481 LPAFGVWVLSFRADNPGAMLFCHIHAMVSGGLGVVYLERADDLRGASVADADDDRLC 540
 QY 541 ADMRRYWPVTPYKSDSGLKHRYVEGEMLYKA 573
 DB 541 ADMRRYWPVTPYKSDSGLKHRYVEGEMLYKA 573

RESULT 15

ID AAM79077 standard; protein; 573 AA.

XX AAM79077;

DT 08-DEC-1998 (first entry)

XX Myceliophthora thermophila laccase mutant.

XX DE laccase; mutant; mutagenesis; detergent; bleaching; textile;
 XX KM lignin modification; polymerisation; phenol; dyeing.

XX Myceliophthora thermophila.

XX Key Location/Qualifiers

FT Misc-difference 106 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 108 /note- "Xaa can be optionally replaced by Ile, Leu,
 FT Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 109 /note- "Xaa can be optionally replaced by Ala, Gln,
 FT Ile, Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 428 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 500 /note- "Xaa can be optionally replaced by Ile, Phe,
 FT Trp, Tyr"

FT Misc-difference 510 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 511 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

FT Misc-difference 514 /note- "Xaa can be optionally replaced by Ala, Ile,
 FT Leu, Phe, Pro, Trp, Tyr, Val"

AC AAW76317;
 XX 08-JAN-1999 (first entry)
 DT
 XX Myceliophthora thermophila-laccase protein variant.
 DE
 XX Laccase; variant; oxidation; dye transfer inhibition; bleaching;
 KM denim; lignin modification; paper strengthening; phenol polymerisation;
 KW hair dye; waste water treatment.
 XX
 OS Synthetic.
 XX Myceliophthora thermophila.
 FH Key Location/Qualifiers
 FT Misc-difference 93 /label= H93E
 FT /note= "optional"
 FT Misc-difference 95 /label= H95E
 FT /note= "optional"
 FT Misc-difference 109 /label= N109D
 FT /note= "optional"
 FT Misc-difference 433 /label= M433E
 FT /note= "optional"
 FT Misc-difference 480 /label= M480E
 FT /note= "optional"
 FT Misc-difference 506 /label= A506E
 FT /note= "optional"
 FT
 XX W09838287-AI.
 XX 03-SEP-1998.
 PD
 XX 23-FEB-1998; 98WO-DK00070.
 XX
 XX 28-FEB-1997; 97DK-0000222.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Svendsen A, Xu F;
 XX
 DR WPI; 1998-495393/42.
 XX
 PT New variants of Coprinus and related laccases with increased
 PT oxidation potential - or altered pH optimum, or mediator or
 PT oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting
 PT dye transfer and in bleaching textiles, especially as detergent
 PT additive
 XX
 PS Claim 18; Page -; 147pp; English.
 XX
 CC The present sequence represents a mutant laccase protein. The
 CC specification describes active laccase variants (see AAW76282,
 CC AAW76296-99 and AAW76316-17) having increased oxidation potential,
 CC altered pH optimum, altered mediator and/or altered oxygen/hydroxide
 CC ion pathway. The laccase variants are used specifically to oxidise
 CC substrates to inhibit dye transfer, and for bleaching textiles,
 CC specifically denim. They can also be used for lignin modification,
 CC strengthening paper, polymerisation of phenols, dyeing of hair and
 CC textiles and waste water treatment.
 CC note: the present sequence does not appear in the specification; it was
 CC constructed using information provided.
 XX
 SO Sequence 573 AA;

QY 1 QOSCTPSNRACWTGDIINTDYEVDSPTGVVRPYTLTLEVDNMTGPDGVKEKVALY 60
 DB 1 QOSCTPSNRACWTDGYINTDYEVDSPTGVVRPYTLTLEVDNMTGPDGVKEKVALY 60
 QY 61 NNSITIGPTIFADMGDTIOIVVNNLEFNGTSHHMHGKQKTNLHDGANGITECPPIPKG 120
 DB 61 NNSITIGPTIFADMGDTIOIVVNNLEFNGTSHHMHGKQKTNLHDGANGITECPPIPKG 120
 QY 121 GRKYRFRKAQGYGTSWHSHESAQYGNVGAIOINGASLPYOTDLGVFTISDYIYSSA 180
 DB 121 GRKYRFRKAQGYGTSWHSHESAQYGNVGAIOINGASLPYOTDLGVFTISDYIYSSA 180
 QY 181 DELVELTRKNSGAPESDNYLFNGTAKHPETGGEYANVTLPGRHRLRLTISVENHPOV 240
 DB 181 DELVELTRKNSGAPESDNYLFNGTAKHPETGGEYANVTLPGRHRLRLTISVENHPOV 240
 QY 241 SLVNHMCIIAADVPVNAATVDSLFLGVGGRYDVIEANPTPGNYVFTFGGGLCGG 300
 DB 241 SLVNHMCIIAADVPVNAATVDSLFLGVGGRYDVIEANPTPGNYVFTFGGGLCGG 300
 QY 301 SRNPYPALIFHYAGAPGPPDESKAPVDHNCIDLPLKPVVARDVPLSGAKRADNTLD 360
 DB 301 SRNPYPALIFHYAGAPGPPDESKAPVDHNCIDLPLKPVVARDVPLSGAKRADNTLD 360
 QY 361 VTLDTGTPLEFVKVNGSAINIDMGRAVDVYLTONTSEFPFGYNIIVENGADOMSYMLIE 420
 DB 361 VTLDTGTPLEFVKVNGSAINIDMGRAVDVYLTONTSEFPFGYNIIVENGADOMSYMLIE 420
 QY 421 NDCGAPFTLPHPHLHGDFYVLGRSPDESPASNERHYFDPARDAGLISGANPVROVSM 480
 DB 421 NDCGAPFTLPHPHLHGDFYVLGRSPDESPASNERHYFDPARDAGLISGANPVROVSE 480
 QY 481 LPFGWVVLSEFRADNPGAMLFHCHIAHVSGLGVYTLERADDLRGAVSDADADDLRLC 540
 DB 481 LPFGWVVLSEFRADNPGAMLFHCHIEHVSGLGVYTLERADDLRGAVSDADADDLRLC 540
 QY 541 ADMRRYPTNPYPRKSDGSLKRWVEEGEWLYKA 573
 DB 541 ADMRRYPTNPYPRKSDGSLKRWVEEGEWLYKA 573
 RESULT 13
 AAW79078
 ID AAW79078 standard; protein; 573 AA.
 XX
 AC AAW79078;
 XX
 XX 08-DEC-1998 (first entry)
 DT
 XX Myceliophthora thermophila laccase mutant.
 DE
 XX Laccase; mutant; mutagenesis; detergent; bleaching; textile;
 KM lignin modification; polymerisation; phenol; dyeing.
 XX
 OS Myceliophthora thermophila.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 93 /note= "M1D-type His substituted by Glu"
 FT Misc-difference 95 /note= "M1D-type His substituted by Glu"
 FT Misc-difference 109 /note= "M1D-type Asn substituted by Asp"
 FT Misc-difference 433 /note= "M1D-type Met substituted by Glu"
 FT Misc-difference 480 /note= "M1D-type Met substituted by Glu"
 FT Misc-difference 506 /note= "M1D-type Met substituted by Glu"
 FT /note= "M1D-type Ala substituted by Glu"
 FT
 XX W09838286-AI.
 XX 03-SEP-1998.

PA (BERK/) BERKA R M.
 PA (WAHL/) WAHLEITHNER J A.
 XX
 PI Berka RM, Feng X, Wahleithner JA;
 XX
 DR WPI; 2000-021805/02.
 DR N-PSDB; AA224236.
 XX
 PT Mutant Rhizoctonia laccase enzymes useful for the polymerization and
 PT depolymerization of lignin -
 XX
 PS Example 9; Column 39-42; 43pp; English.
 XX
 CC This invention describes novel mutant Rhizoctonia solani laccase enzymes
 CC modified to exhibit altered characteristics (e.g. pH activity profile)
 CC relative to the wild-type enzyme. The mutant enzymes have a number of
 CC commercial and industrial applications. For example, they may be used for
 CC the polymerization of lignin (both Kraft and lignosulfates) in solution
 CC to produce high molecular weight lignin. They may also be used for the in
 CC situ depolymerization of lignin in Kraft pulp to produce low molecular
 CC weight lignin. They may also be used for the polymerization of phenolic
 CC or aniline compounds in liquids (for example apple juice may be treated
 CC with the enzyme to accelerate precipitation of the phenolic compounds in
 CC the juice to stabilize it). Additionally, it may be used to decolorize
 CC dyes and dye precursors by oxidation. The mutant laccase enzymes exhibit
 CC different characteristics to those of the wild-type enzyme. In
 CC particular, they may exhibit an altered pH activity profile relative to
 CC the wild-type enzyme or altered specific activities. Additionally, they
 CC may be produced in large quantities. This sequence represents the
 CC Myceliophthora thermophila laccase protein lcc-1.
 CC
 XX
 SQ Sequence 620 AA;
 Query Match 100.0%; Score 3158; DB 21; Length 620;
 Best Local Similarity 100.0%; Pred. No. 8.5e-276;
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QOSCTPSNRACWTDGYDINTDYEVDSPDGVVRYTLTLEVDNMWTPGCVVKEKMLV 60
 DB 48 QOSCTPSNRACWTDGYDINTDYEVDSPDGVVRYTLTLEVDNMWTPGCVVKEKMLV 107
 QY 61 NNSLTGPTIPADMGDTIQVYINNLFTNGTSHWGLHOKGTNLHDGANGTECPIDPKG 120
 DB 108 NNSLTGPTIPADMGDTIQVYINNLFTNGTSHWGLHOKGTNLHDGANGTECPIDPKG 167
 QY 121 GRKYRKAQOYGSWYSHSFAOYGVGVAIOINGPASPYPDTDLGVEPISDYSSA 180
 DB 168 GRKYRKAQOYGSWYSHSFAOYGVGVAIOINGPASPYPDTDLGVEPISDYSSA 227
 QY 181 DELVELTKNSGAPSDVNLFGTAKHETGEGEYANTLTPGRHRRLRLINTSVENHFQV 240
 DB 228 DELVELTKNSGAPSDVNLFGTAKHETGEGEYANTLTPGRHRRLRLINTSVENHFQV 287
 QY 241 SLVNHHTCIIAADMVPVNAATVDSLFGVGRVDYVTEANFTPGNTYFNTFGGGLCGG 300
 DB 288 SLVNHHTCIIAADMVPVNAATVDSLFGVGRVDYVTEANFTPGNTYFNTFGGGLCGG 347
 QY 301 SRNYPPIAFYAGAPGPPDEKAPVDHNCIDLPLMKPVAVADVLSGPAKADNTLD 360
 DB 348 SRNYPPIAFYAGAPGPPDEKAPVDHNCIDLPLMKPVAVADVLSGPAKADNTLD 407
 QY 361 VTLDITGTPLEFWRKVSAINIDMGRAVDVYLQNTSFPFGYNIIVEVNGADMSWYLE 420
 DB 408 VTLDITGTPLEFWRKVSAINIDMGRAVDVYLQNTSFPFGYNIIVEVNGADMSWYLE 467
 QY 421 NDEPAPPTLPHPHLHGHDYVYGRSPDESASNERHVPAPRACGLLSGANPRRVSM 480
 DB 468 NDEPAPPTLPHPHLHGHDYVYGRSPDESASNERHVPAPRACGLLSGANPRRVSM 527
 QY 481 LPAFGVVLSEFRADNPGAWLFEHCHIAHWVSGGLGVYLERADDLRGVAVSADADDDLRLC 540
 DB 528 LPAFGVVLSEFRADNPGAWLFEHCHIAHWVSGGLGVYLERADDLRGVAVSADADDDLRLC 587

QY 541 ADMRRYPTNPYPKSDSGLKRHWEEGEMLYKA 573
 DB 588 ADMRRYPTNPYPKSDSGLKRHWEEGEMLYKA 620
 RESULT 10
 ID AAW79079 standard; protein: 573 AA.
 XX
 AC AAW79079;
 XX
 DT 08-DEC-1998 (first entry)
 XX
 DE Myceliophthora thermophila laccase mutant.
 XX
 KW Laccase; mutant; mutagenesis; detergent; bleaching; textile;
 XX lignin modification; polymerisation; phenol; dyeing.
 OS Myceliophthora thermophila.
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 189
 FT /note= "Xaa can be optionally replaced by Ala, Gly, Ser,
 FT Thr"
 FT Misc-difference 190
 FT /note= "Xaa can be optionally replaced by Ala, Gly"
 FT Misc-difference 371
 FT /note= "Xaa can be optionally deleted or replaced by Ala,
 FT Gly"
 FT Misc-difference 218
 FT label=unknown
 FT Misc-difference 234
 FT label=unknown
 FT Misc-difference 557
 FT label=unknown
 XX
 PN WO9838286-A1.
 PD 03-SEP-1998.
 XX
 PF 20-FEB-1998; 98WO-DK00067.
 XX
 PR 28-FEB-1997; 97DK-0000221.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Svendsen A;
 XX
 DR WPI; 1998-495392/42.
 XX
 PT New variants of laccase with increased oxidation potential - or
 PT altered pH optimum, mediator efficiency or oxygen hydroxide ion
 PT pathways, useful for oxidation, inhibiting dye transfer and in
 PT textile bleaching
 PS
 XX
 Disclosure; Page -: 34pp; English.
 XX
 CC The laccase protein mutants AAW79077-W79079 contain one or more of the
 CC above substitutions and are examples of polypeptides modified from the
 CC wild-type sequence by using site-directed, random, or localised random
 CC mutagenesis. These mutants may have an (a) increased oxidation
 CC potential, (b) altered pH optimum, (c) altered mediator efficiency, (d)
 CC altered oxygen/hydroxide ion pathway, depending on the particular
 CC mutations that have occurred. This particular sequence has mutations
 CC that will alter the laccase's oxygen/hydrogen ion pathway. These
 CC variants can be used to oxidise substrates, inhibit dye transfer, as
 CC detergent additives and bleaching textiles. They can also be used in
 CC lignin modification; strengthening paper; polymerisation of phenols;
 CC dyeing of hair and textiles and waste water treatment.
 CC N.B. This sequence is not shown in the specification but is derived
 CC from the wild-type Myceliophthora thermophila laccase sequence given in
 CC the specification.

Query Match 100.0%; Score 3158; DB 21; Length 573;
 Best Local Similarity 100.0%; Pred. No. 7.6e-276;
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QQSCNTPSNRACWTDGIDINTDYEVDSPDGVVARYTLTLEVDNMTPGPGVYKEXKMLV 60
DB 1 QQSCNTPSNRACWTDGIDINTDYEVDSPDGVVARYTLTLEVDNMTPGPGVYKEXKMLV 60
QY 61 NNSIIGPTIFADMGDTIQVTVINNLETNGTSIHMHGKHOKGTNLHDGANGITECPPIPKG 120
DB 61 NNSIIGPTIFADMGDTIQVTVINNLETNGTSIHMHGKHOKGTNLHDGANGITECPPIPKG 120
QY 121 GRRYRERKAAQOYGTSMYSHSFAQYNGVGAIDINGPASLPYDTDLGVEPIDSYSSA 180
DB 121 GRRYRERKAAQOYGTSMYSHSFAQYNGVGAIDINGPASLPYDTDLGVEPIDSYSSA 180
QY 181 DELVELTKNSGAPPSDNLNGTAKHETEGEYANTTLTGRHRRLRLINTSVENHFQY 240
DB 181 DELVELTKNSGAPPSDNLNGTAKHETEGEYANTTLTGRHRRLRLINTSVENHFQY 240
QY 241 SLVNHPTCIIAADVPVNAATVDSLFLGVGORYDVTEANRTPGNMYFNTPFGGILCGG 300
DB 241 SLVNHPTCIIAADVPVNAATVDSLFLGVGORYDVTEANRTPGNMYFNTPFGGILCGG 300
QY 301 SRNPYPALIFHYAGAPGPPTEDEKAPVDHNCIDLPLMKPVVARDVPLSGFAKRAADNTLD 360
DB 301 SRNPYPALIFHYAGAPGPPTEDEKAPVDHNCIDLPLMKPVVARDVPLSGFAKRAADNTLD 360
QY 361 VTLDITGTPLFVWKVNGSAINIDMGRAVDVYLQNTSFPFGYNIIVEANGADQMSYWLIE 420
DB 361 VTLDITGTPLFVWKVNGSAINIDMGRAVDVYLQNTSFPFGYNIIVEANGADQMSYWLIE 420
QY 421 NDGCAPTTLPHPHLHGHDFYVLCRSPDESPASNERHVPFDPARDAGLLSGANPYRDVSM 480
DB 421 NDGCAPTTLPHPHLHGHDFYVLCRSPDESPASNERHVPFDPARDAGLLSGANPYRDVSM 480
QY 481 LPAFGVYVLSFRADNPGAMLFHCHIAHNVSGGLGVYLERADLRGAVSADADDLRLC 540
DB 481 LPAFGVYVLSFRADNPGAMLFHCHIAHNVSGGLGVYLERADLRGAVSADADDLRLC 540
QY 541 ADMRRYWPNTNYPKSDGSLKRWVEEGEWLYKA 573
DB 541 ADMRRYWPNTNYPKSDGSLKRWVEEGEWLYKA 573

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RESULT 7
 AAR88500
 ID AAR88500 standard; Protein; 620 AA.

AC AAR88500;
 DT 28-MAR-1996 (first entry)
 XX

DE Myceliophthora laccase enzyme.
 XX
 XX Laccase; lignin degradation; delignification; depolymerisation;
 KM Kraft pulp; waste-water; soil detoxification; hair dye;
 XX
 XX Myceliophthora thermophila.
 OS
 XX
 XX W09533836-A1.
 PN
 XX
 XX 14-DEC-1995.
 PD
 XX
 XX 31-MAY-1995; 95MO-US06815.
 PF
 XX
 XX 15-MAY-1995; 95US-0441146.
 PR
 XX 03-JUN-1994; 94US-0253781.
 XX
 XX (NOVO) NOVO NORDISK BIOTECH INC.
 PA
 XX (NOVO) NOVO-NORDISK AS..
 XX

PI Aaslyng DA, Berka RM, Brown SH, Oxenboll KM, Schneider P;
 PI Xu F;
 XX
 XX WPI; 1996-058139/06.
 DR N-PSDB; AAT10922.
 XX
 XX DNA encoding a Myceliophthora laccase enzyme - used in hair dye
 PT compositions, to reduce the use of hydrogen peroxide and improve
 PT hair condition
 XX
 XX Claim 8; Page 41-43; 58pp; English.
 PS
 XX The Myceliophthora thermophila laccase (AAR88500) is the product
 CC of a gene (AAT10922) isolated from a genomic library using the
 CC Neurospora crassa laccase gene (lcc1) as probe. The enzyme is
 CC capable of lignin modification, Kraft mill pulp depolymerisation,
 CC soil detoxification, and of dyeing hair. Recombinant laccase can be
 CC produced in a prokaryotic or eukaryotic, pref. Aspergillus, host.
 XX

Sequence 620 AA;

Query Match 100.0%; Score 3158; DB 17; Length 620;
 Best Local Similarity 100.0%; Pred. No. 8.5e-276;
 Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QQSCNTPSNRACWTDGIDINTDYEVDSPDGVVARYTLTLEVDNMTPGPGVYKEXKMLV 60
DB 48 QQSCNTPSNRACWTDGIDINTDYEVDSPDGVVARYTLTLEVDNMTPGPGVYKEXKMLV 107
QY 61 NNSIIGPTIFADMGDTIQVTVINNLETNGTSIHMHGKHOKGTNLHDGANGITECPPIPKG 120
DB 61 NNSIIGPTIFADMGDTIQVTVINNLETNGTSIHMHGKHOKGTNLHDGANGITECPPIPKG 120
QY 108 NNSIIGPTIFADMGDTIQVTVINNLETNGTSIHMHGKHOKGTNLHDGANGITECPPIPKG 167
DB 108 NNSIIGPTIFADMGDTIQVTVINNLETNGTSIHMHGKHOKGTNLHDGANGITECPPIPKG 167
QY 121 GRRYRERKAAQOYGTSMYSHSFAQYNGVGAIDINGPASLPYDTDLGVEPIDSYSSA 180
DB 121 GRRYRERKAAQOYGTSMYSHSFAQYNGVGAIDINGPASLPYDTDLGVEPIDSYSSA 180
QY 168 GRRYRERKAAQOYGTSMYSHSFAQYNGVGAIDINGPASLPYDTDLGVEPIDSYSSA 227
DB 168 GRRYRERKAAQOYGTSMYSHSFAQYNGVGAIDINGPASLPYDTDLGVEPIDSYSSA 227
QY 181 DELVELTKNSGAPPSDNLNGTAKHETEGEYANTTLTGRHRRLRLINTSVENHFQY 240
DB 181 DELVELTKNSGAPPSDNLNGTAKHETEGEYANTTLTGRHRRLRLINTSVENHFQY 240
QY 228 DELVELTKNSGAPPSDNLNGTAKHETEGEYANTTLTGRHRRLRLINTSVENHFQY 287
DB 228 DELVELTKNSGAPPSDNLNGTAKHETEGEYANTTLTGRHRRLRLINTSVENHFQY 287
QY 241 SLVNHPTCIIAADVPVNAATVDSLFLGVGORYDVTEANRTPGNMYFNTPFGGILCGG 300
DB 241 SLVNHPTCIIAADVPVNAATVDSLFLGVGORYDVTEANRTPGNMYFNTPFGGILCGG 300
QY 288 SLVNHPTCIIAADVPVNAATVDSLFLGVGORYDVTEANRTPGNMYFNTPFGGILCGG 347
DB 288 SLVNHPTCIIAADVPVNAATVDSLFLGVGORYDVTEANRTPGNMYFNTPFGGILCGG 347
QY 301 SRNPYPALIFHYAGAPGPPTEDEKAPVDHNCIDLPLMKPVVARDVPLSGFAKRAADNTLD 360
DB 301 SRNPYPALIFHYAGAPGPPTEDEKAPVDHNCIDLPLMKPVVARDVPLSGFAKRAADNTLD 360
QY 348 SRNPYPALIFHYAGAPGPPTEDEKAPVDHNCIDLPLMKPVVARDVPLSGFAKRAADNTLD 407
DB 348 SRNPYPALIFHYAGAPGPPTEDEKAPVDHNCIDLPLMKPVVARDVPLSGFAKRAADNTLD 407
QY 361 VTLDITGTPLFVWKVNGSAINIDMGRAVDVYLQNTSFPFGYNIIVEANGADQMSYWLIE 420
DB 361 VTLDITGTPLFVWKVNGSAINIDMGRAVDVYLQNTSFPFGYNIIVEANGADQMSYWLIE 420
QY 408 VTLDITGTPLFVWKVNGSAINIDMGRAVDVYLQNTSFPFGYNIIVEANGADQMSYWLIE 467
DB 408 VTLDITGTPLFVWKVNGSAINIDMGRAVDVYLQNTSFPFGYNIIVEANGADQMSYWLIE 467
QY 421 NDGCAPTTLPHPHLHGHDFYVLCRSPDESPASNERHVPFDPARDAGLLSGANPYRDVSM 480
DB 421 NDGCAPTTLPHPHLHGHDFYVLCRSPDESPASNERHVPFDPARDAGLLSGANPYRDVSM 480
QY 468 NDGCAPTTLPHPHLHGHDFYVLCRSPDESPASNERHVPFDPARDAGLLSGANPYRDVSM 527
DB 468 NDGCAPTTLPHPHLHGHDFYVLCRSPDESPASNERHVPFDPARDAGLLSGANPYRDVSM 527
QY 481 LPAFGVYVLSFRADNPGAMLFHCHIAHNVSGGLGVYLERADLRGAVSADADDLRLC 540
DB 481 LPAFGVYVLSFRADNPGAMLFHCHIAHNVSGGLGVYLERADLRGAVSADADDLRLC 540
QY 528 LPAFGVYVLSFRADNPGAMLFHCHIAHNVSGGLGVYLERADLRGAVSADADDLRLC 587
DB 528 LPAFGVYVLSFRADNPGAMLFHCHIAHNVSGGLGVYLERADLRGAVSADADDLRLC 587
QY 541 ADMRRYWPNTNYPKSDGSLKRWVEEGEWLYKA 573
DB 541 ADMRRYWPNTNYPKSDGSLKRWVEEGEWLYKA 573

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RESULT 8
 AAM16302
 ID AAM16302 standard; Protein; 620 AA.

AC AAM16302;
 DT 07-AUG-1997 (first entry)
 XX

|||||
DB 421 NDPAFTLPHMLHGHDEYVLCGRSPDESPASNERHVPDPARAGLLSGANPVRDYSM 480
OY 481 LPAFGVVLSPFRADNPGAMLPHCHIAHVSGLGVYVLERADDLRGAVSDADDLRLC 540
DB 481 LPAFGVVLSPFRADNPGAMLPHCHIAHVSGLGVYVLERADDLRGAVSDADDLRLC 540
OY 541 ADMRRVWPTNPYPRKSDGLKRWVEEGEMLYKA 573
DB 541 ADMRRVWPTNPYPRKSDGLKRWVEEGEMLYKA 573
RESULT 4
AAM51782
ID AAM51782 standard; peptide; 573 AA.
XX
AC AAM51782;
XX
DT 12-OCT-1998 (first entry)
XX
DE Myceliophthora thermophila laccase protein.
XX
KM Laccase protein; variant; lignin modification; paper strengthening;
KM dye transfer inhibition; phenol2 polymerisation; hair dyeing;
KM textile bleaching; denim; waste water treatment.
XX
OS Myceliophthora thermophila.
FH Key Location/Qualifiers
FT misc_difference 136 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 137 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 145 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 176 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 254 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 373 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 433 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 480 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
FT misc_difference 507 /note- "optionally replaced with Ala, Val, Leu,
FT Ile, Pro, Phe, Trp, Gly, Ser, Thr, Cys,
FT Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His"
PN MO9827197-A1.
XX
PD 25-JUN-1998.
XX
PF 12-DEC-1997; 97WO-DK00566.
XX
PR 08-SEP-1997; 97DK-0001020.

PR 19-DEC-1996; 96DK-0001450.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Cherry JR, Pedersen AH, Rasmussen G, Schneider P;
PI Svendsen A;
XX
DR WPI; 1998-362767/31.
XX
PT New laccase variants - have amino acid changes in Myceliophthora or
PT Scytalidium laccase(s), used for e.g. oxidation, dye transfer
PT inhibition or bleaching
XX
PS Claim 1; Pages 18-21; 30pp; English.
XX
CC The present sequence represents a laccase protein. The sequence is used
CC to construct laccase variants which have improved stability as compared
CC to the parent laccase, and comprises a mutation in tyrosine, tryptophan
CC or methionine residues. The laccase variants can be used for e.g. lignin
CC modification, paper strengthening, dye transfer inhibition in detergents,
CC phenol polymerisation, hair dyeing, bleaching of textiles (in particular
CC bleaching of denim) and waste water treatment.
XX
SQ Sequence 573 AA;
Query Match 100.0%; Score 3158; DB 19; Length 573;
Best Local Similarity 100.0%; Pred. No. 7.6e-276;
Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QOCSNTSPSNRACWTGXDINTDYEDSPDGVNRYTLTLEVDNMTGPDGVREKVMY 60
DB 1 QOCSNTSPSNRACWTGXDINTDYEDSPDGVNRYTLTLEVDNMTGPDGVREKVMY 60
OY 61 NNSITGPTIRADWCDTQYVYINLLETNGTSIHMHGLOKSTNHDGANGTECPDPPKG 120
DB 61 NNSITGPTIRADWCDTQYVYINLLETNGTSIHMHGLOKSTNHDGANGTECPDPPKG 120
OY 121 GRKYRFRKAOYGTSMYSHSFAOYGVNGVGAIOINGPASLPYTDGVPFISDYSSA 180
DB 121 GRKYRFRKAOYGTSMYSHSFAOYGVNGVGAIOINGPASLPYTDGVPFISDYSSA 180
OY 181 DELVELTKNSGAPPSDVLNLTNGTAKHPETGEGEYANTLTGRRHRLRLINTSVENHFQY 240
DB 181 DELVELTKNSGAPPSDVLNLTNGTAKHPETGEGEYANTLTGRRHRLRLINTSVENHFQY 240
OY 241 SLVNHMCITIAADVPVNAATVDSLFVGGORGVYVLEANTPENVYENYTFGGGLCGG 300
DB 241 SLVNHMCITIAADVPVNAATVDSLFVGGORGVYVLEANTPENVYENYTFGGGLCGG 300
OY 301 SRNFPYPAIFHYAGAPGPTDEKARVDHNCIDLPLKRPVAVDVLGFAKRAADNTLD 360
DB 301 SRNFPYPAIFHYAGAPGPTDEKARVDHNCIDLPLKRPVAVDVLGFAKRAADNTLD 360
OY 361 VTIIDTGTPTPLFVWKVNSAINIDMGRAVDYVLTQNTSPPGVIYVYVNGADQSYLTIE 420
DB 361 VTIIDTGTPTPLFVWKVNSAINIDMGRAVDYVLTQNTSPPGVIYVYVNGADQSYLTIE 420
OY 421 NDPAFTLPHMLHGHDEYVLCGRSPDESPASNERHVPDPARAGLLSGANPVRDYSM 480
DB 421 NDPAFTLPHMLHGHDEYVLCGRSPDESPASNERHVPDPARAGLLSGANPVRDYSM 480
OY 481 LPAFGVVLSPFRADNPGAMLPHCHIAHVSGLGVYVLERADDLRGAVSDADDLRLC 540
DB 481 LPAFGVVLSPFRADNPGAMLPHCHIAHVSGLGVYVLERADDLRGAVSDADDLRLC 540
OY 541 ADMRRVWPTNPYPRKSDGLKRWVEEGEMLYKA 573
DB 541 ADMRRVWPTNPYPRKSDGLKRWVEEGEMLYKA 573
RESULT 5
AAM63124
ID AAM63124 standard; peptide; 573 AA.

| Pr | dy | transfer | and | in | bleaching | textiles, | especially | as | detergent | additive |
|----|-----|--|-------------|--------------|------------|------------------|------------|------------|---------------|---------------|
| PS | XX | Disclosure: | Pages | 133-134; | 147pp; | English. | | | | |
| CC | XX | The | present | sequence | represents | a | laccase | protein. | The | specification |
| CC | CC | describes | active | laccase | variants | (see | AAW6282, | AAW6296-99 | and | CC |
| CC | CC | AAW6316-17) | having | increased | oxidation | potential, | altered | pH | optimum, | CC |
| CC | CC | altered | mediator | and/or | altered | oxygen/hydroxide | ion | pathway. | The | CC |
| CC | CC | laccase | variants | are | used | specifically | to | oxidise | substrates, | to |
| CC | CC | inhibit | dye | transfer, | and | for | bleaching | textiles, | specifically | denim. |
| CC | CC | They | can | also | be | used | for | lignin | modification, | strengthening |
| CC | CC | polymerisation | of | phenols, | dyeing | of | hair | and | textiles | and |
| CC | CC | waste | treatment. | | | | | | | |
| XX | XX | Sequence | 573 | AA: | | | | | | |
| XX | XX | Query | Match | 100.0%; | Score | 3158; | DB | 19; | Length | 573; |
| XX | XX | Best | Local | Similarity | 100.0%; | Pred. | No. | 7.6e-276; | | |
| XX | XX | Matches | 573; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps |
| OY | 1 | OOSCTPNSRAACMTGCGDINTDYEVDSPRTGVRRPTLTLTEDNMNTGSDGVYKKEVMY | 60 | | | | | | | |
| DB | 1 | OOSCTPNSRAACMTGCGDINTDYEVDSPRTGVRRPTLTLTEDNMNTGSDGVYKKEVMY | 60 | | | | | | | |
| OY | 61 | NNSIIGPTTFADMGDTIOYTVININLETNGTSHMHGKHOKGTVLHMGANGITECPRPKG | 120 | | | | | | | |
| DB | 61 | NNSIIGPTTFADMGDTIOYTVININLETNGTSHMHGKHOKGTVLHMGANGITECPRPKG | 120 | | | | | | | |
| OY | 121 | GKKYVRFRKAQOCTSMYHSHFSAQYGVNGVYGAIOINGRPSLPRDTDLGYFPISDIYSSA | 180 | | | | | | | |
| DB | 121 | GKKYVRFRKAQOCTSMYHSHFSAQYGVNGVYGAIOINGRPSLPRDTDLGYFPISDIYSSA | 180 | | | | | | | |
| OY | 181 | DELVELTKNSGAFPSDNVLFNGTAKHPETEGEREYANVTLPGRHRRLRLINTSVENHFOY | 240 | | | | | | | |
| DB | 181 | DELVELTKNSGAFPSDNVLFNGTAKHPETEGEREYANVTLPGRHRRLRLINTSVENHFOY | 240 | | | | | | | |
| OY | 241 | SLVNHNTMCIADAMPVYNAATYDSLFLGIGORYDYVTEANRPFGNTWVNTFGGGLCGG | 300 | | | | | | | |
| DB | 241 | SLVNHNTMCIADAMPVYNAATYDSLFLGIGORYDYVTEANRPFGNTWVNTFGGGLCGG | 300 | | | | | | | |
| OY | 301 | SNRPALAFHAGAGGPGPTDEGKAPVYHNCIDLPNLKPVYARQVPLSGPAKRADNTLD | 360 | | | | | | | |
| DB | 301 | SNRPALAFHAGAGGPGPTDEGKAPVYHNCIDLPNLKPVYARQVPLSGPAKRADNTLD | 360 | | | | | | | |
| OY | 361 | VLDTTGTGPELFYWKVNGSAINIDMGRAVVDYVLTONTSPPEGYNIVEVNGADQWSYMLE | 420 | | | | | | | |
| DB | 361 | VLDTTGTGPELFYWKVNGSAINIDMGRAVVDYVLTONTSPPEGYNIVEVNGADQWSYMLE | 420 | | | | | | | |
| OY | 421 | NDGPGAFPLPHMHMLHGHEFYVLGRSPDSPAENSEHNVDPARADGLLSGAPVRRDYSM | 480 | | | | | | | |
| DB | 421 | NDGPGAFPLPHMHMLHGHEFYVLGRSPDSPAENSEHNVDPARADGLLSGAPVRRDYSM | 480 | | | | | | | |
| OY | 481 | LPAFGVMVLSFRADNPGAWLFFCHCIAMHVSGGIGVYTERADDLRGAVSDAADDLDRIC | 540 | | | | | | | |
| DB | 481 | LPAFGVMVLSFRADNPGAWLFFCHCIAMHVSGGIGVYTERADDLRGAVSDAADDLDRIC | 540 | | | | | | | |
| OY | 541 | ADMRRYVPTNPYPKSDSGLKHWRVEEGEVLVKA | 573 | | | | | | | |
| DB | 541 | ADMRRYVPTNPYPKSDSGLKHWRVEEGEVLVKA | 573 | | | | | | | |
| XX | XX | RESULT 2 | | | | | | | | |
| XX | XX | AAW5913 | | | | | | | | |
| XX | XX | AAW59913 | standard; | protein; | 573 | AA. | | | | |
| XX | XX | AAW59913; | | | | | | | | |
| XX | XX | 08-DEC-1998 | (first | entry) | | | | | | |
| XX | XX | Myceliophthora | thermophila | laccase | protein. | | | | | |
| XX | XX | laccase; | mutant; | mutagenesis; | detergent; | bleaching; | textile; | | | |

| | |
|----|--|
| KM | Lignin modification; polymerisation; phenol; dyeing. |
| XX | Myceliophthora thermophila. |
| OS | WO9638286-A1. |
| PN | 03-SEP-1998. |
| PD | 20-FEB-1998; |
| XX | 98WO-DK00067. |
| PF | 28-FEB-1997; |
| XX | 97DK-0000221. |
| PR | (NOVO) NOVO-NORDISK AS. |
| XX | Svendsen A; |
| PI | WPI; 1998-495392/42. |
| DR | New variants of laccase with increased oxidation potential - or altered pH optimum, mediator efficiency or oxygen-hydroxide ion pathways, useful for oxidation, inhibiting dye transfer and in textile bleaching |
| PT | Claim 2; Page 17-20; 34pp; English. |
| XX | This sequence represents a M. thermophila laccase wild-type polypeptide. This sequence can be used to generate laccase mutants, by using site-directed, random, or localised random mutagenesis. These mutants may have an (a) increased oxidation potential, (b) altered pH optimum, (c) altered mediator efficiency, (d) altered oxygen/hydroxide ion pathway, depending on the particular mutations that have occurred. These variants can be used to oxidise substrates, inhibit dye transfer, as detergent additives and bleaching textiles. They can also be used in lignin modification; strengthening paper; polymerisation of phenols; dyeing of hair and textiles and waste water treatment. |
| CC | Sequence 573 AA; |
| SO | Query Match 100.0%; Score 3158; DB 19; Length 573; Best Local Similarity 100.0%; Pred. No. 7.6e-276; Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| OY | 1 QOQCFTPSNRACWTDGCIYDINDIYEVDSPTDGVRPPYTLLTEVDMWTGPDGVKKERMLY 60 |
| PB | 1 QOQCFTPSNRACWTDGCIYDINDIYEVDSPTDGVRPPYTLLTEVDMWTGPDGVKKERMLY 60 |
| OY | 61 NNSIIIGPITFADMGDTIOVTYNNLETNGTSLHMHGLHOKGNLMDGANGITECPRPKG 120 |
| PB | 61 NNSIIIGPITFADMGDTIOVTYNNLETNGTSLHMHGLHOKGNLMDGANGITECPRPKG 120 |
| OY | 121 GKRYTRFAQQGYGISWYSHSFSAQYGNGVGAIQINGPASLPDYDTDLGVFPISDIYYSSA 180 |
| PB | 121 GKRYTRFAQQGYGISWYSHSFSAQYGNGVGAIQINGPASLPDYDTDLGVFPISDIYYSSA 180 |
| OY | 181 DELVELTFKNSGAFSDNVLNFNGTAHPHEEGSEEVANNLTTPERRRRRLRLINISVNHQY 240 |
| PB | 181 DELVELTFKNSGAFSDNVLNFNGTAHPHEEGSEEVANNLTTPERRRRRLRLINISVNHQY 240 |
| OY | 241 SLVNHTMCIIAADMPVPVNAMTVDLSFLGAGQGYDVAVIEANRTPGMYWFNTFGSGILLCGG 300 |
| PB | 241 SLVNHTMCIIAADMPVPVNAMTVDLSFLGAGQGYDVAVIEANRTPGMYWFNTFGSGILLCGG 300 |
| OY | 301 SRNPRAALIFHYAGAPGGPPDEGAAPVDHNCILD.PNLKPVARADVPLISGFPAKRADNTLD 360 |
| PB | 301 SRNPRAALIFHYAGAPGGPPDEGAAPVDHNCILD.PNLKPVARADVPLISGFPAKRADNTLD 360 |
| OY | 361 VTLDTGTGPLFELFWKNKNSAINIDMGRAVVDDYVLTONTSEFPPEYNIVVENGADOMSTYLIE 420 |
| PB | 361 VTLDTGTGPLFELFWKNKNSAINIDMGRAVVDDYVLTONTSEFPPEYNIVVENGADOMSTYLIE 420 |
| OY | 421 NDPCAPFLPLPRPMHLHGHDIFYVLGSPPDESASNERHVPDPARDAAGLLSGANPVRRDYSM 480 |
| PB | 421 NDPCAPFLPLPRPMHLHGHDIFYVLGSPPDESASNERHVPDPARDAAGLLSGANPVRRDYSM 480 |